

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 FNNFTVSFWLRVPKVSASHLEG 38
Db 133 FNNFTVSFWLRVPKVSASHLEG 154

RESULT 12
Sequence 59, Application US/10295074
Publication No US20030185845A1
GENERAL INFORMATION:
APPLICANT: Pharmexa A/S
TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILE REFERENCE: P1013DK00
CURRENT APPLICATION NUMBER: US/10/295,074
CURRENT FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
SEQ ID NO 47
LENGTH: 194
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: htnf with inserted tetanus toxoid p2 and p30 epitopes

Qy 18 FNNFTVSFWLRVPKVSASHLEG 38
Db 133 FNNFTVSFWLRVPKVSASHLEG 154

RESULT 13
Sequence 2, Application US/10297942
Publication No. US20030185816A1
GENERAL INFORMATION:
APPLICANT: Ferring BV
TITLE OF INVENTION: Solubilised Protein Vaccines
FILE REFERENCE: P68445US0
CURRENT APPLICATION NUMBER: US/10/297,942
CURRENT FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: PCT/DK01/00431
PRIOR FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: DK PA 2000 00966
PRIOR FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 158
TYPE: PRT
ORGANISM: Homo sapiens

Qy 19 FNNFTVSFWLRVPKVSASHLEG 38
Db 133 FNNFTVSFWLRVPKVSASHLEG 154

RESULT 14
Sequence 47, Application US/10295074
Publication No. US20030185845A1
GENERAL INFORMATION:
APPLICANT: Pharmexa A/S

Qy 20 FNNFTVSFWLRVPKVSASHLEG 38
Db 133 FNNFTVSFWLRVPKVSASHLEG 154

Query Match 42.3%; Score 116; DB 14; Length 158;
Best Local Similarity 100%; Pred. No. 1.0e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 FNNFTVSFWLRVPKVSASHLEG 37
Db 133 FNNFTVSFWLRVPKVSASHLEG 154

Query Match 41.1%; Score 114; DB 14; Length 158;
Best Local Similarity 70.5%; Pred. No. 2.8e-06;
Matches 24; Conservative 0; Mismatches 2; Indels 8; Gaps 1;

Qy 22 FNNFTVSFWLRVPKVSASHLEG 37
Db 133 FNNFTVSFWLRVPKVSASHLEG 154

Search completed: March 10, 2004, 10:25:49
Job time : 39.2996 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 10, 2004, 08:58:54 ; Search time 14.6304 Seconds
(without alignments)
309.015 Million cell updates/sec

Title: US-09-848-834A-17
Perfect score: 248
Sequence: 1 XHMSYGLRPSSGPSLKLULS.....HRLEGVEGPSLHHWSYGLRXP 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : PIR 78:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	72	29.0	282	2	PQ0376		cell fusion glycoprotein - measles virus (strain Schwarz vaccine) (fragment)
2	72	29.0	282	2	PQ0388		cell fusion glycop
3	72	29.0	534	1	JU0274		cell fusion glycop
4	72	29.0	546	2	JU4730		cell fusion glycop
5	72	29.0	550	1	E48556		cell fusion glycop
6	72	29.0	553	1	VGNMZM		cell fusion glycop
7	71	28.6	546	1	VGNZRK		cell fusion glycop
8	71	28.6	546	2	S47035		gene F Protein - r
9	66.5	26.8	552	2	S47034		cell fusion protein
10	66	26.6	542	2	JQ2223		protein
11	66	26.6	546	1	VGNZRL		cell fusion glycop
12	66	26.6	662	1	VGNZCD		cell fusion glycop
13	66	26.6	662	2	S21382		cell fusion protein
14	65	26.2	631	1	VGNZDD		cell fusion glycop
15	65	26.2	631	2	A48346		cell fusion glycop
16	64	25.8	67	1	RHHUG		gonadotropin prec
17	64	25.8	92	1	RHHUG		gonadotropin prec
18	63.5	25.6	98	2	I50739		gonadotropin-relea
19	62.5	25.2	89	2	I51423		gonadotropin prec
20	60.5	24.4	82	2	I51465		gonadotropin-relea
21	60.5	24.4	555	2	B72486		probable hydantoin
22	60.5	24.4	880	2	B53743		protein-tyrosine k
23	60	24.2	546	2	S55386		cell fusion protein
24	59.5	24.0	90	1	REMSG		gonadotropin prec
25	59.5	24.0	1041	2	C83548		hypothetical prote
26	58.5	23.6	502	2	T36599		probable transmembr
27	58	23.4	10	1	RHGG		gonadotropin - pi
28	58	23.4	10	1	RHSHG		gonadotropin prec
29	58	23.4	92	1	RHRHG		

ALIGNMENTS

RESULT 1

PQ0376
cell fusion glycoprotein - measles virus (strain TT) (fragment)
C;Species: measles virus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Nov-1999
C;Accession: PQ0376
R;Schulz, T.F.; Head, J.G.; Whityb, D.; Tizard, E.J.; Dillon, M.J.; Weiss, R.A.
J; Gen. Virol. 73, 1581-1586, 1992
A;Title: A measles virus isolate from a child with Kawasaki disease: sequence comparison
A;Reference number: PQ0374; PMID:92300360; PMID:1607874
A;Accession: PQ0376
A;Residues: 1-282 <SCH>
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion

Query Match % Score 72; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match % Score 72; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

PQ0388
cell fusion glycoprotein - measles virus
C;Species: measles virus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Nov-1999
C;Accession: PQ0388
R;Schulz, T.F.; Head, J.G.; Whityb, D.; Tizard, E.J.; Dillon, M.J.; Weiss, R.A.
J; Gen. Virol. 73, 1581-1586, 1992
A;Title: A measles virus isolate from a child with Kawasaki disease: sequence comparison
A;Reference number: PQ0374; PMID:92300360; PMID:1607874
A;Accession: PQ0388
A;Residues: 1-282 <SCH>
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion

Query Match % Score 72; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match % Score 72; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match % Score 72; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

JU0274 cell fusion glycoprotein precursor - subacute sclerosing panencephalitis virus (strain Y) N; Contains: fusion glycoprotein F1; fusion Glycoprotein F2 C; Species: subacute sclerosing panencephalitis virus, SSBV C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000 R; Komase, K.; Haga, T.; Yoshikawa, Y.; Sato, T.A.; Yamamotochi, K.

A; Title: Molecular analysis of structural protein genes of the Yamagata-1 strain of defe A; Reference number: JU0274; PMID:169327; MUID:90385702; NCBI:129274

A; Accession: JU0274

A; Molecule type: mRNA

A; Residues: 1-534 <KOM>

A; Cross-references: EMBL:D10548; PIDN:BA01405.1; PIDN:9222256; PIDN:BA01405.1; PIDN:9222257

A; Note: the authors translated the codon GTR for residue 459 as Gly and GGG for residue 460

C; Genetics:

A; Gene: F

C; Superfamily: paramyovirus cell fusion protein

C; Keywords: Glycoprotein; membrane fusion; transmembrane protein

C; /Keywords: Glycoprotein; membrane fusion; transmembrane protein

C; /22/Domain: signal sequence #status Predicted <SG>

F; 23-107/Product: cell fusion Glycoprotein F2 #status Predicted <FF2>

F; 108-550/Product: cell fusion Glycoprotein F1 #status Predicted <FF1>

F; 6-29-61/Domain: transmembrane #status Predicted <TM>

F; 6-29-61/67/Binding site: carbohydrate (Abn) (covalent) #status Predicted <TM>

Query Match 29.0%; Score 72; DB 1; Length 550;

Best Local Similarity 100.0%; Pred. No. 0.5%; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LSEIKGVIVHLLEGV 33

Db 288 LSEIKGVIVHLLEGV 302

RESULT 6

VGNZMV

cell Fusion Glycoprotein precursor - measles virus

C; Species: measles virus

C; Date: 31-Mar-1988 #sequence_revision 31-Mar-1989 #text_change 16-Jun-2000

C; Accession: A29592; A25616; PQ0380; PQ0384

R; Buckland, R.; Gerald, C.; Barker, R.; Wild, T.F.

J. Gen. Virol. 68, 1695-1703, 1987

A; Title: Fusion glycoprotein sequence of measles virus: nucleotide sequence of the gene and comp

A; Reference number: A92794; PMID:3585281

A; Accession: A26162

A; Molecule type: mRNA

A; Residues: 1-553 <BU>

A; Cross-references: GB:D00090; NID:9222061; PIDN:BAA00056.1; PIDN:9222062

A; Experimental source: strain Halle

R; Richardson, C.; Hull, D.; Greer, P.; Hasel, K.; Berkovich, A.; Englund, G.; Bellini,

Virology 155, 508-522, 1986

A; Title: The nucleotide sequence of the mRNA encoding the fusion protein of measles vir

A; Reference number: A94350; MUID:87224816; PMID:3585281

A; Accession: A2616

A; Molecule type: mRNA

A; Residues: 4-553 <RIC>

A; Cross references: GB:W14915; NID:9331762; PIDN:AAA46423.1; PIDN:9331763

A; Experimental source: strain Edmonston

R; Schutz, T.F.; Roode, J.G.; Whiby, D.; Tizard, E.J.; Dillon, M.J.; Weiss, R.A.

J. Gen. Virol. 73, 1581-1586, 1992

A; Title: A measles virus isolate from a child with Kawasaki disease: sequence comparisc

A; Reference number: PQ0374; MUID:92300360; PMID:1607874

A; Accession: PQ0380

A; Molecule type: genomic RNA

A; Residues: 272-553 <SCH1>

A; Experimental source: isolate CL

A; Accession: PQ0384

A; Molecule type: genomic RNA

A; Residues: 272-553 <SCH2>

A; Experimental source: isolate SE

C; Genetics:

A; Gene: F

C; Superfamily: paramyovirus cell fusion protein

C; Keywords: Glycoprotein; membrane fusion; transmembrane protein

C; /22/Domain: signal sequence #status Predicted <SG>

F; 23-107/Product: cell fusion Glycoprotein F2 #status Predicted <FF2>

F; 108-550/Product: cell fusion Glycoprotein F1 #status Predicted <FF1>

Query Match 29.0%; Score 72; DB 2; Length 546;

Best Local Similarity 100.0%; Pred. No. 0.5%; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LSEIKGVIVHLLEGV 33

Db 284 LSEIKGVIVHLLEGV 298

RESULT 5

C;Keywords: glycoprotein; membrane fusion; transmembrane protein.

F;1:25/#Domain: signal sequence #status predicted <SIG>

F;26:110/Product: cell fusion Glycoprotein F2 #status predicted <FF2>

F;111-553/Product: cell fusion Glycoprotein F1 #status predicted <FF1>

F;501-51/#Domain: transmembrane #status Predicted <TMN>

F;32:64,70/Binding site: carbohydrate (Asn) (covalent) #status Predicted

Query Match 29.0%; Score 72; DB 1; Length 553;

Best Local Similarity 100.0%; Pred. No. 52; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0;

Qy 19 LSEIKGVIVHRLGEV 33

Db 291 LSEIKGVIVHRLGEV 305

RESULT 7

VGNRK cell fusion glycoprotein precursor - rinderpest virus (strain Kabete O)

N:Contains: fusion Glycoprotein F1; fusion Glycoprotein F2

C;Species: rinderpest virus

C;Accession: S47034

R;Hu, D.; Yamamoto, M.; Miller, J.; Dale, B.; Grubman, M.; Yilmaz, T.

A;Title: Cloning of the fusion gene of rinderpest virus: comparative sequence analysis

A;Reference number: A31051; PMID:3413983

A;Accession: A31051

A;Molecule type: genomic RNA

C;Genetics:

A;Gene: F

C;Superfamily: parainfluenza virus cell fusion protein

C;Keywords: glycoprotein; membrane fusion; transmembrane protein

F;1:19/#Domain: signal sequence #status predicted <SIG>

F;20-108/Product: cell fusion Glycoprotein F2 #status predicted <FF2>

F;109-546/Product: cell fusion Glycoprotein F1 #status predicted <FF1>

F;1:09-134/#Domain: transmembrane #status Predicted <TN1>

F;491-513/#Domain: transmembrane #status Predicted <TN2>

F;25,51,52,53,54/Binding site: carbohydrate (Asn) (covalent) #status Predicted

Query Match 28.6%; Score 71; DB 1; Length 546;

Best Local Similarity 93.3%; Pred. No. 0.68; Gaps 0;

Matches 14; Conservative 1; Mismatches 0; Indels 0;

Qy 19 LSEIKGVIVHRLGEV 33

Db 284 LSEIKGVIVHRLGEV 298

RESULT 8

S47305 Gene F protein - rinderpest virus

C;Species: rinderpest virus

C;Accession: S47305; S47301

R;Barrett, M.D.; Barrett, T.

A;Submitted to the EMBL Data Library, March 1994

A;Description: The sequence of the N and L genes of Rinderpest virus, and the 50 and 30

A;Reference number: S47283

A;Accession: S47305

A;Molecule type: mRNA

C;Superfamily: parainfluenza virus cell fusion protein

C;Keywords: transmembrane protein

F;1:20-Oct-1994 #sequence_revision 08-Sep-1995 #text_change 20-Sep-1999

P;Barn, M.D.; Barrett, T.

A;Cross-references: EMBL:Z10697; PID:9535396; PID:CAA83181.1; PID:9535401; EMBL:Z30700;

Query Match 28.6%; Score 71; DB 2; Length 546;

Best Local Similarity 93.3%; Pred. No. 0.68; Gaps 0;

Matches 14; Conservative 1; Mismatches 1; Indels 0;

Qy 19 LSEIKGVIVHRLGEV 33

Db 276 SYPTLSVEKSVIVRLEAV 294

RESULT 11

Db 284 LSEIKGVIVHRLGEV 298

RESULT 9

S47034 cell fusion protein precursor - porpoise morbillivirus

N:Alternate names: F protein

C;Species: porpoise morbillivirus

C;Accession: S47034

R;Bolt, G.; Gottschalk, E.; Blixenkrone-Møller, M.; Wishaupt, R.G.A.; Welsh, M.J.H.

A;Description: Nucleotide sequence comparisons of the F and M genes of cetacean morbillivirus

A;Reference number: S47034

A;Accession: S47034

A;Molecule type: mRNA

A;Residues: 1-552 <SQL>

A;Cross-references: EMBL:X80757; PID:9520639; PID:CA56731.1; PMID:9520640

A;Experimental source: isolate Ulster 88

A;Note: the source is designated Cetacean morbillivirus

C;Superfamily: parainfluenza virus cell fusion protein

F;1-25/#Domain: signal sequence #status Predicted <SIG>

F;26-55/#Product: fusion protein #status Predicted <MAT>

Query Match 26.5%; Score 66.5%; DB 2; Length 552;

Best Local Similarity 61.5%; Pred. No. 2.5;

Matches 16; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

Qy 19 LSEIKGVIVHRLGEVPSLHWYSTL 44

Db 290 LSEVKGVIVHRLAEV -----SYNL 308

RESULT 10

JQ2223 cell fusion protein F0 precursor - phocine distemper virus

N:Contains: F1 and F2 chains

C;Species: phocine distemper virus

C;Accession: JQ2223

R;Visser, I.K.G.; van der Heijden, R.W.J.; van de Bildt, M.W.G.; Kenter, M.J.H.; Oerve

J.Gen.Virol. 74, 1989-1994, 1993

A;Title: Fusion protein gene nucleotide sequence similarities, shared antigenic sites

e virus entity.

A;Reference number: JQ2223; PMID:93389459; PMID:8376973

A;Accession: JQ2223

A;Molecule type: mRNA

A;Residues: 1-542 <VIS>

A;Cross-references: GB:L07075

A;Note: the authors translated the codon ATC for residue 4 as Leu

C;Comment: This fusion protein F0 is cleaved into F1 and F2 chains.

C;Genetics:

A;Gene: F

C;Superfamily: parainfluenza virus cell fusion protein

C;Keywords: glycoprotein; membrane fusion; transmembrane protein

F;1-15/#Domain: signal sequence #status Predicted <SIG>

F;16-52/#Product: Fusion protein #status Predicted <MAT>

F;16-59/#Product: F2 chain #status Predicted <FC2>

F;105-542/#Product: F1 chain #status Predicted <FC1>

P;105-135/#Region: hydrophobic

P;21,53,59,397/Binding site: carbohydrate (Asn) (covalent) #status Predicted

Query Match 26.6%; Score 66.5%; DB 2; Length 542;

Best Local Similarity 73.7%; Pred. No. 2.8;

Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 15 SUKLSEIKGVIVHRLLEGV 33

Db 276 SYPTLSVEKSVIVRLEAV 294

RESULT 11

VGNZRL
cell fusion glycoprotein precursor - rinderpest virus (strain L)
N: Contains: fusion glycoprotein F1; fusion glycoprotein F2
C: Species: rinderpest virus
C: Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
R: Tsukiyama, K.; Yoshihikawa, Y.; Yamamoto, K.
A: Title: Fusion glycoprotein (F) of rinderpest virus: entire nucleotide sequence of the Virology 164: 523-520, 1988
A: Cross-references: GB:M20870; PIDN:AAA47399.1; PMID:g333899
A: Residues: 1-546 <TSU>
A: Molecule type: mRNA
A: Genetics:
A: Gene: F
C: Superfamily: parainfluenza virus cell fusion protein
C: Keywords: Glycoprotein; membrane fusion; transmembrane protein
F: A1-19:Domain: signal sequence #status Predicted <SIG>
F: 20-104/Product: cell fusion glycoprotein F1 #status Predicted <FG1>
F: 105-346/Product: cell fusion glycoprotein F1 #status Predicted <FG2>
F: 109-133/Domain: transmembrane #status Predicted <TM1>
F: 185-513/Domain: transmembrane #status Predicted <TM2>
F: 25-57/Domain: carbohydrate (Amn) (covalent) #status Predicted <RN2>
P: 25, 57/3/Binding site: carbohydrate site #status Predicted <RN1>
P: 25, 57/3/Binding site: carboxylate site #status Predicted <TN2>

Query Match Score 66; DB 1; Length 546;
Best Local Similarity 93.3%; Pred. No. 2.8%;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 LSEIKGVIVHRLLEGV 33
Db 284 LSEIKGVIVHRLLEVS 298

RESULT 12
VGNZCD
cell fusion glycoprotein precursor - canine distemper virus
N: Contains: fusion protein F1; fusion protein F2
C: Species: canine distemper virus
C: Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C: Accession: JS0321
R: Barrett, T.; Clarke, D.K.; Evans, S.A.; Rima, B.K.
A: Title: The nucleotide sequence of the gene encoding the F protein of canine distemper A: Reference number: JS0321; MUID:88129050; PMID:3433924
A: Accession: JS0321
A: Residues: 1-662 <BAR>
A: Cross-references: GB:M21849; PIDN:AAA42878.1; PMID:g323242
A: Molecule type: mRNA
A: Genetics:
A: Gene: F
C: Superfamily: parainfluenza virus cell fusion protein
C: Keywords: Glycoprotein; membrane fusion; transmembrane protein
F: 1-135/Domain: signal sequence #status Predicted <SIG>
F: 136-224/Product: cell fusion glycoprotein F2 #status Predicted <F2P>
F: 225-662/Product: cell fusion glycoprotein F1 #status Predicted <F1P>
F: 62-141:173-179,517/Binding site: carbohydrate (Asn) (covalent) #status Predicted <HEM>

Query Match Score 66; DB 1; Length 662;
Best Local Similarity 73.7%; Pred. No. 3.5%;
Matches 14; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 15 SLKLSEIKGVIVHRLLEGV 33
Db 396 SYPTLSEVKGVIVHRLLEAV 414

RESULT 13
S21382
cell fusion protein - canine distemper virus
C: Species: canine distemper virus
C: Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999

C: Accession: S21382
R: Wild, T.F.; Bernard, A.; Spohner, D.; Villeval, D.; Drillien, R.
A: Description: Vaccination of mice against canine distemper virus induced encephalitis submitted to the EMBL Data Library, April 1992
A: Reference number: S21382
A: Accession: S21382
A: Status: preliminary
A: Molecule type: Genomic RNA
A: Residues: 1-662 <WIL>
A: Cross-references: EMBL:X65509; PIDN:CAA6481.1; PMID:g58854
C: Superfamily: parainfluenza virus cell fusion protein
Query Match Score 66; DB 2; Length 662;
Best Local Similarity 73.7%; Pred. No. 3.5%;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 15 SLKLSEIKGVIVHRLLEGV 33
Db 396 SYPTLSEVKGVIVHRLLEAV 414

RESULT 14
VGNZPD
cell fusion glycoprotein precursor - Phocine distemper virus
C: Contains: fusion protein F1; fusion protein F2
C: Species: Phocine distemper virus
C: Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 25-Oct-1996
R: Roeverans, J.; Blixenkrone-Møller, M.; Sharma, B.; Oervell, C.; Norby, E.
J: Gen. Virol. 72, 2953-2966, 1991
A: Title: The nucleotide sequence and deduced amino acid composition of the haemagglutinin A: Reference number: QJ1368; MUID:92113538; PMID:1765768
A: Accession: QJ1368
A: Molecule type: Genomic RNA
A: Residues: 1-631 <KOV>
C: Genetics:
A: Gene: F
C: Superfamily: parainfluenza virus cell fusion protein
C: Keywords: glycoprotein; membrane fusion; transmembrane protein
F: 1-188/Product: cell fusion glycoprotein F2 #status Predicted <FP2>
F: 89-106/Domain: transmembrane #status Predicted <TM1>
F: 189-192/Region: cleavage processing #status Predicted <FP1>
F: 193-631/Product: cell fusion glycoprotein F1 #status Predicted <TM2>
F: 194-212/Domain: transmembrane #status Predicted <TM3>
F: 575-595/Domain: transmembrane #status Predicted <TM4>
F: 110-142:148-486/Binding site: carbonylate (Asn) (covalent) #status Predicted <COVALEN>
P: 110-142:148-486/Binding site: carbonylate (Asn) (covalent) #status Predicted <COVALEN>

Query Match Score 65; DB 1; Length 631;
Best Local Similarity 66.4%; Pred. No. 4.4%;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 15 SLKLSEIKGVIVHRLLEGV 33
Db 365 SYPTLSEVKGVIVHRLLEAV 383

RESULT 15
A8346
cell fusion glycoprotein precursor - phocine distemper virus (strain Ulster/88)
N: Contains: fusion protein F1; fusion protein F2
C: Species: Phocine distemper virus
C: Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 25-Oct-1996
R: Curran, M.D.; Lu, Y.J.; Rima, B.K.
A: Title: The fusion protein gene of phocine distemper virus: nucleotide and deduced ami
A: Reference number: A48346; MUID:92398837; PMID:1524494
A: Accession: A8346
A: Molecule type: mRNA
A: Residues: 1-631 <CUR>
A: Note: sequence extracted from NCBI backbone (NCBIN:113098, NCBI:113099)
C: Genetics:
A: Gene: F

C;Superfamily: Parainfluenza virus cell fusion protein
C;Keywords: Glycoprotein; membrane fusion; transmembrane protein
P;1-188/Product: cell fusion glycoprotein P0 #status predicted <FP2>
P;89-106/Domain: transmembrane #status predicted <TM1>
P;194-631/Product: cell fusion glycoprotein F1 #status predicted <FP1>
P;194-219/Domain: cell fusion glycoprotein F1 #status predicted <TM2>
P;575-595/Domain: transmembrane #status predicted <TM3>
P;110,142/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.2%; Score 65; DB 1; Length 631;
Best Local Similarity 68.4%; Pred. No. 4.4;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 15 SLKILSEIKEVIVRLEGV 33
Db 365 SYPTLSEVKGVVHRLEAV 383

Search completed: March 10, 2004, 09:16:51
Job time : 14.6892 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:53 ; Search time 0.59533 Seconds

(without alignments)
284.724 Million cell updates/sec

Title: US-09-848-834A-17

Perfect score: 248

Sequence: 1 XHNSYGLRFGSSGPSLKLIS.....HRLEGYEGPSLHWMSYGLRXP 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	72.5	29.2	95	1	GONI_SPAU	P51919 sparaxis aurata
2	72	29.0	534	1	VGLF_MESE	P26032 meles meles vir
3	72	29.0	546	1	VGLF_RINDB	P41360 rinderpest
4	72	29.0	550	1	VGLF_MEASA	P235973 meles meles vir
5	72	29.0	550	1	VGLF_MESE	P083000 meles meles vir
6	71	28.6	546	1	VGLF_RINDR	P41356 rinderpest
7	68.5	27.6	95	1	GONI_PAGNA	P70074 pagrus major
8	66	26.6	546	1	VGLF_RINDL	P10864 rinderpest
9	66	26.6	662	1	VGLF_CDVO	P12569 canine dist
10	65	26.2	546	1	VGLF_RINDR	P12574 rinderpest
11	65	26.2	631	1	VGLF_PHODY	P28886 phocine dist
12	64	25.8	67	1	GONI_MACMU	P55247 macaca mulatta
13	64	25.8	92	1	GONI_HUMAN	P0148 homo sapiens
14	64	25.8	529	1	VGLF_MEASI	P6031 meles meles vir
15	63.5	25.6	94	1	GONI_HAPBU	P1918 haplochromis
16	62.5	25.2	89	1	GONI_XENILLA	P45566 xenopus laevis
17	61.5	24.8	61	1	GONI_SHEEP	Q25588 ovis aries
18	60.5	24.4	74	1	GONI_ONCMY	P25246 oncorhynchus
19	60.5	24.4	82	1	GONI_SALTR	P55653 salmo trutta
20	60.5	24.4	169	1	CX41_THUOB	Q91800 thymus obliquus
21	60.5	24.4	880	1	TYO3_MOUSE	P93335 tupaias glis
22	60	24.2	92	1	GONI_TUPGB	P35562 mus musculus
23	59.5	24.0	90	1	GONI_MOUSE	P9921 sus scrofa
24	59.5	23.8	95	1	GONI_PIG	O33812 morone saxatilis
25	58	23.4	63	1	GONI_MESAU	O99163 mesocirrhites
26	58	23.4	23.4	1	GONI_RANCA	Q9y63 ratus catesbeianus
27	58	23.4	90	1	GONI_RAT	P07490 ratus norvegicus
28	58	23.4	92	1	GONI_DICLIA	Q9ia10 dicentrarchus
29	58	23.4	99	1	TYO3 RAT	TYO3 rat
30	57.5	23.2	880	1	GONI_ONCTS	Q9a097 oncorhynchus
31	56.5	22.8	74	1	GONI_SALSA	P35629 salmo salar
32	56.5	22.8	82	1	MTRD_METH	O72230 methanobacter
33	55.5	22.4	233	1	PROGONADOLIBERIN	PROGONADOLIBERIN I.

ALIGNMENTS

RESULT 1	GONI_SPAU	STANDARD;	PRT;	95 AA.
ID	GONI_SPAU			
AC	P51919;			
DT	01-OCT-1996	(Rel. 34, Created)		
DT	01-OCT-1996	(Rel. 34, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Gonadoliberin I precursor (Gonadotropin-releasing hormone I) (GNRH-I)			
DE	(LH RH I) (Lutiberin I) (SBGnRH).			
GN	GNRH.			
OS	Sparus aurata (Gilthead sea bream).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Pecidoidei; Acanthomorpha; Acanthopterygii; Perciformes; Percidae; Sparidae; Sparus.			
OC	OC			
OC	NCBI TaxID=8175;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RC	MEDLINE=5268499; PubMed=7749463.			
RA	Gothilf Y., Elizur A., Chow M., Chen T.T., Zohar Y.;			
RA	"Molecular cloning and characterization of a novel gonadotropin-releasing hormone from the Gilthead seabream (<i>Sparus aurata</i>).";			
RA	RT			
RA	"Three forms of gonadotropin-releasing hormone characterized from brains of one species".			
RT	RT			
RT	Proc. Natl. Acad. Sci. U.S.A. 91:12081-12085 (1994).			
RL	RT			
RL	FUNCTION: Stimulates the secretion of gonadotropins.			
CC	-1- SUBCELLULAR LOCATION: Mitochondria.			
CC	-1- MASS SPECTROMETRY: MW=1113.6; METHOD=MALDI; RANGE=26-35.			
CC	-1- SIMILARITY: Belongs to the GNRH Family.			
CC	--			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/) or send an email to license@isb-sib.ch.			
CC	--			
CC	InterPro; IPR004079; Gonadoliberini.			
DR	InterPro; IPR002012; GnrH.			
DR	PRINTS; PRO1541; GONADOLIBRNT.			
DR	INTERPRO; PS00473; GNRH.			
KW	Cleavage on pair of basic residues: Hormone; Amidation; Hypothalamus; Signal; Multigene Family; Pyrrolidone carboxylic acid.			
FT	SIGNAL 1			
FT	CHAIN 26			
FT	25			
FT	95			

FT	PEPTIDE	26	35	GONADOLIBERIN I, GNRH-ASSOCIATED PEPTIDE I (POTENTIAL).		Best Local Similarity 100.0%; Pred. No. 0.13; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT	PEPTIDE	39	95	PYROIDONE PYROXYNIC ACID.		
FT	MOD RES	26	26	AMIDATION (G-36 PROVIDE AMIDE GROUP).		
FT	MOD RES	35	35	49312FD6FB77DA CRC64;		
SQ	SEQUENCE	95 AA:	10753 MW:			
Query Match		29.2%	Score 72.5; DB 1; Length 95;			
Matches 16; Consistency 45.7%; Pred. No. 0.016; Indels 1; Gaps 1;						
2 HWSYGLRGSSGPSSLKLUSEIKGVTLRVEGQP 36			RESULT 3	VGLF_RINDB STANDARD; PRT; 546 AA.		
3 HWSYGLSGFGK-RDLDLSDTIGNITERPHVDS 60			ID VGLF_RINDB	AC P41360; DT 01-FBB-1995 (Rel. 31, Created)		
Query Match		22.1%	Score 72.5; DB 1; Length 95;	OS Rinderpest virus (strain RTBL) (RDV).		
Matches 16; Consistency 45.7%; Pred. No. 0.016; Indels 1; Gaps 1;			OC Viruses; ssRNA negative-strand viruses; Mononegavirales;			
2 HWSYGLRGSSGPSSLKLUSEIKGVTLRVEGQP 36			OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.			
3 HWSYGLSGFGK-RDLDLSDTIGNITERPHVDS 60			GN F	RN [1] _TAXID=39007;		
Query Match		22.1%	Score 72.5; DB 1; Length 95;	RP SEQUENCE FROM N.A. PubMed=7996154;		
Matches 16; Consistency 45.7%; Pred. No. 0.016; Indels 1; Gaps 1;			RA MEDLINE=508809; RNAME=Baron M.D., Chamberlain R.W., Goatley L., Barrett T.;			
2 HWSYGLRGSSGPSSLKLUSEIKGVTLRVEGQP 36			RT "Nucleotide sequence comparisons of the fusion protein gene from virulent and attenuated strains of rinderpest virus."			
3 HWSYGLSGFGK-RDLDLSDTIGNITERPHVDS 60			RL J. Gen. Virol. 75:3611-3617(1994).			
Query Match		22.1%	Score 72.5; DB 1; Length 95;	CC -1- FUNCTION: This protein directs fusion of viral and cellular membranes.		
Matches 16; Consistency 45.7%; Pred. No. 0.016; Indels 1; Gaps 1;			CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2 LINKED BY A DISULFIDE BOND.			
2 HWSYGLRGSSGPSSLKLUSEIKGVTLRVEGQP 36			CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein family.			
3 HWSYGLSGFGK-RDLDLSDTIGNITERPHVDS 60			CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.			
Query Match		22.1%	Score 72.5; DB 1; Length 95;	CC CC "Nucleotide sequence of structural protein genes of the Yamagata-1 strain of defective subacute sclerosing panencephalitis virus. IV. Virus Genes 4:173-181(1999)."		
Matches 16; Consistency 45.7%; Pred. No. 0.016; Indels 1; Gaps 1;			CC CC -1- FUNCTION: This protein directs fusion of viral and cellular membranes.			
2 HWSYGLRGSSGPSSLKLUSEIKGVTLRVEGQP 36			CC CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2 LINKED BY A DISULFIDE BOND.			
3 HWSYGLSGFGK-RDLDLSDTIGNITERPHVDS 60			CC CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein family.			
Query Match		22.1%	Score 72.5; DB 1; Length 95;	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
Matches 16; Consistency 45.7%; Pred. No. 0.016; Indels 1; Gaps 1;			CC DR EMBL: D10548; BA01405.1; -.			
2 HWSYGLRGSSGPSSLKLUSEIKGVTLRVEGQP 36			DR PIR: S47300; S47300.			
3 HWSYGLSGFGK-RDLDLSDTIGNITERPHVDS 60			DR HSSP: P04849; 1SVF.			
Query Match		22.1%	Score 72.5; DB 1; Length 95;	DR InterPro: IPR000776; Fusion_gly.		
Matches 16; Consistency 45.7%; Pred. No. 0.016; Indels 1; Gaps 1;			DR Pfam: PF00523; fusion_gly.			
2 HWSYGLRGSSGPSSLKLUSEIKGVTLRVEGQP 36			DR KW Glycoprotein; Fusion_protein; Transmembrane; Envelope_protein; Signal.			
3 HWSYGLSGFGK-RDLDLSDTIGNITERPHVDS 60			FT SIGNAL 1 19 FT CHAIN 20 546 FUSION GLYCOPROTEIN F0.			
Query Match		22.1%	Score 72.5; DB 1; Length 95;	FT FT PROTEIN.		
Matches 16; Consistency 45.7%; Pred. No. 0.016; Indels 1; Gaps 1;			FT FT CHAIN 20 108 F2 PROTEIN.			
2 HWSYGLRGSSGPSSLKLUSEIKGVTLRVEGQP 36			FT FT DOMAIN 104 546 ARG/LYS-RICH (BASIC).			
3 HWSYGLSGFGK-RDLDLSDTIGNITERPHVDS 60			FT FT TRANSMEM 109 133 POTENTIAL.			
Query Match		22.1%	Score 72.5; DB 1; Length 95;	FT FT DOMAIN 484 513 POTENTIAL.		
Matches 16; Consistency 45.7%; Pred. No. 0.016; Indels 1; Gaps 1;			FT FT TRANSMEM 514 517 ARG/LYS-RICH (BASIC).			
2 HWSYGLRGSSGPSSLKLUSEIKGVTLRVEGQP 36			FT FT DISULFID 64 191 LINKAGE BETWEEN F2 & F1 (POTENTIAL).			
3 HWSYGLSGFGK-RDLDLSDTIGNITERPHVDS 60			FT FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).			
Query Match		22.1%	Score 72.5; DB 1; Length 95;	FT FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).		
Matches 16; Consistency 45.7%; Pred. No. 0.016; Indels 1; Gaps 1;			FT FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).			
2 HWSYGLRGSSGPSSLKLUSEIKGVTLRVEGQP 36			FT FT CARBOHYD 518 518 O-LINKED (POTENTIAL).			
3 HWSYGLSGFGK-RDLDLSDTIGNITERPHVDS 60			FT SQ SEQUENCE 546 AA; 58418 MW; 38B539B89344F01 CRC64;			
Query Match		22.1%	Score 72.5; DB 1; Length 95;	DR Query Match 29.0%; Score 72; DB 1; Length 534;		
Matches 16; Consistency 45.7%; Pred. No. 0.016; Indels 1; Gaps 1;			DR Best Local Similarity 100.0%; Pred. No. 0.13; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
2 HWSYGLRGSSGPSSLKLUSEIKGVTLRVEGQP 36			DR 19 LSEIKGIVVHLREGV 33			
3 HWSYGLSGFGK-RDLDLSDTIGNITERPHVDS 60			DR 284 LSEIKGIVVHLREGV 298			

RESULT 4

VGLF_MEASA	STANDARD;	PRT;	550 AA.
ID			
AC	P35971;		
DT	01-JUN-1994 (Rel. 29, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Fusion glycoprotein precursor [Contains: Fusion glycoprotein F1; Fusion Glycoprotein F1].		
GN	F.		
OS	Measles virus (strain Edmonston) (Subacute sclerose panencephalitis virus).		
OC	Measles virus (strain Halle) (Subacute sclerose panencephalitis virus).		
OC	Measles virus (strain Leningrad-16) (Subacute sclerose panencephalitis virus).		
OC	Measles virus (strain Edmonston-Zagreb) (Subacute sclerose panencephalitis virus).		
OC	Measles virus (strain Philadelphia-26) (Subacute sclerose panencephalitis virus).		
OC	Measles virus (strain Edmonston B) (Subacute sclerose panencephalitis virus).		
OC	ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Morbilliviruses; NCBI_TAXID=36401;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
XX	MLINE=93227570; PubMed=8470368;		
RA	Mori T., Sasaki K., Hashimoto H., Makino S., "Molecular cloning and complete nucleotide sequence of genomic RNA of the A/K-C strain of attenuated measles virus.", Virus Genes 7:67-81(1993).		
RT	"The protein directs fusion of viral and cellular membranes.		
CC	-!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2 LINKED BY A DISULFIDE BOND.		
CC	-!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein family.		
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licence agreement (See http://www.isb-sib.ch/announce/CC or send an email to license@isb-sib.ch).		
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licence agreement (See http://www.isb-sib.ch/announce/CC or send an email to license@isb-sib.ch).		
CC	DR EMBL: S58415; AB26145.1; PIR: E49556; E49556; A98949; ISVP; DR InterPro: IPR000776; Fusion glycoprotein; PFam: PF00523; fusion_glycan_domain; KW Glycoprotein; Fusion_protein; Transmembrane; Envelope_protein; Signal_peptide; SIGNAL 1 23		
FT	CHAIN 24 550 FUSION GLYCOPROTEIN F0.		
FT	CHAIN 24 112 PROTEIN F2.		
FT	CHAIN 113 550 PROTEIN F2.		
FT	TRANSEM 113 136 POTENTIAL.		
FT	TRANSEM 137 494 EXTRACELLULAR (POTENTIAL).		
FT	TRANSEM 495 515 POTENTIAL.		
FT	DOMAIN 516 550 CYTOPLASMIC (POTENTIAL).		
FT	DISULFD 68 195 LINKAGE BETWEEN F2 & F1 (POTENTIAL).		
FT	CARBOND 29 29 N-LINKED (GLCNAC, . .) (POTENTIAL).		
FT	CARBOND 61 67 N-LINKED (GLCNAC, . .) (POTENTIAL).		
FT	CARBOND 67 67 N-LINKED (GLCNAC, . .) (POTENTIAL).		
SQ	SEQUENCE 550 AA; 59540 MW; AACDAB92DE0D938 CRC64;		

Query Match 29.0%; Score 72; DB 1; Length 550;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5

VGLF_MEASE	STANDARD;	PRT;	550 AA.
ID	PO8300;		
AC	AC_01-AUG-1988 (Rel. 08, Created)		
DT	01-AUG-1988 (Rel. 08, Last sequence update)		

Qy 19 LSEIKGVTHRLLEGV 33
 Db 288 LSEIKGVTHRLLEGV 302

--!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GnRH family.

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CC EMBL; M20870; AAAA47399.1; -.
 CC DR EMBL; A28921; VENZRL.
 CC DR PIR; A28921; VENZRL.
 CC HSSP9; P04819; ISVF.
 CC DR InterPro; IPR000776; Fusion glycoprotein.
 CC DR Pfam; PF00323; fusion_gly_1.
 CC KW Glycoprotein; Fusion Protein; Transmembrane; Envelope protein; Signal.

CC FT SIGNAL 1 19
 CC FT CHAIN 20 546 FUSION GLYCOPROTEIN F0.
 CC FT CHAIN 20 108 P2 PROTEIN.
 CC FT CHAIN 109 546 P1 PROTEIN.
 CC FT DOMAIN 104 108 ARG/LYS-RICH (BASIC).
 CC FT TRANSMEM 109 133 POTENTIAL.
 CC FT TRANSMEM 484 513 POTENTIAL.
 CC FT DOMAIN 514 191 ARG/LYS-RICH (BASIC).
 CC FT DISULFID 64 191 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
 CC FT CARBOHYD 25 25 N-LINKED (GLCNAC, . .) (POTENTIAL).
 CC FT CARBOHYD 57 57 N-LINKED (GLCNAC, . .) (POTENTIAL).
 CC FT CARBOHYD 63 63 N-LINKED (GLCNAC, . .) (POTENTIAL).
 CC SQ SEQUENCE 546 AA; 985029418P28FFB5 CRC64;

Query Match Score 66; DB 1; Length 546;
 Best Local Similarity 93.3%; Pred. No. 0.78;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC FT PEPTIDE 24 33 PROGONADOLIBERIN I.
 CC FT PEPTIDE 24 33 GNRH ASSOCIATED PEPTIDE I (POTENTIAL).
 CC FT PYRROLIDONE CARBOXYRIC ACID (BY SIMILARITY).
 CC FT AMIDATION (G-34 PROVIDE AMIDE GROUP)
 CC FT MOD_RES 33 33 (BY SIMILARITY).
 CC FT SEQUENCE 95 AA; 10566 MW; 61E71C990328D3E CRC64;

Query Match Score 68.5; DB 1; Length 95;
 Best Local Similarity 42.9%; Pred. No. 0.054;
 Matches 15; Conservative 3; Mismatches 16; Indels 1; Gaps 1;

CC OY 2 HWSYGLPGSSPSPLKLSLEIKGVIVHLRLEVEGP 36
 CC DB 25 HWSYGLSPGGK-RDLDLSDLTDIIFERPHADSP 58

RESULT 8
 VGLF RINDL STANDARD; PRT; 546 AA.
 AC P10865; PubMed=3285575;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 DE Fusion glycoprotein Fl].
 GN P.
 OS Rinderpest virus (strain L) (RDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbilliviridae.
 RN NCBI_TaxID=11243;

SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A. (CDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbilliviridae.
 RN NCBI_TaxID=11233;

RP SEQUENCE FROM N.A.
 RA MEDLINE=88129050; PubMed=2433924;
 RT "The nucleotide sequence of the gene encoding the F protein of canine distemper virus: a comparison of the deduced amino acid sequence with other paramyxoviruses."
 RT Virus Res. 8:373-386(1987).
 RL Virus Res. 8:373-386(1987).
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8821954; PubMed=8470428;
 RA Wild T. F., Bernard A., Spohner D., Villevie-D., Drillien R.;
 RT "Vaccination of mice against canine distemper virus-induced encephalitis with vacinia virus recombinants encoding measles or canine distemper virus antigens.";
 RT Vaccine 11:438-444(1993).
 CC -!- FUNCTION: This protein directs fusion of viral and cellular membranes.
 CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
 CC -!- LINKED BY A DISULFIDE BOND.
 CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein family.
 CC --!- SUBCELLULAR LOCATION: Belongs to the paramyxoviruses fusion glycoprotein family.

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[3] SEQUENCE FROM N.A., AND VARIANT SER-16.
 RP MEDLINE=9012739; PubMed=090931;
 RX PMID=090931;
 RA "Characterization of cDNA for precursor of human luteinizing hormone releasing hormone.";
 RT Nature 311:666-668 (1984).
 [4] SEQUENCE OF 24-33;
 RP MEDLINE=83126573; PubMed=6760865;
 RX PMID=6760865;
 RA Ran L.; Rousseau P.;
 RT "The chemical identity of the immunoreactive LHRH-like peptide biosynthesized in the human placenta.";
 RU Biochim. Biophys. Res. Commun. 109:1061-1071(1982).
 [5] VARIANT SER-16.
 RP MEDLINE=99318093; PubMed=10391209;
 RA Cargill M.; Altshuler D.; Ireland J.; Sklar P.; Ardlie K.; Patil N.;
 Shaw N.; Lane C.R.; Lim E.P.; Kalyanaraman N.; Nemesh J.; Ziaugra L.;
 Friedland L.; Rolfe A.; Warrington J.; Lipschutz R.; Daley G.Q.,
 Landier E.S.;
 RT "Characterization of single-nucleotide polymorphisms in coding regions of human genes.";
 RL Nat. Genet. 22:231-238(1999).
 [6] RN
 RP CERATUM M.; Altshuler D.; Ireland J.; Sklar P.; Ardlie K.; Patil N.,
 RA Shaw N.; Lane C.R.; Lim E.P.; Kalyanaraman N.; Nemesh J.; Ziaugra L.,
 Friedland L.; Rolfe A.; Warrington J.; Lipschutz R.; Daley G.Q.,
 Landier E.S.;
 RA Nat. Genet. 23:373-373(1999).
 CC -|- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.
 CC -|- SUBCELLULAR LOCATION: Secreted
 CC -|- PHARMACEUTICAL: Available under the names Factrel (Ayerst Labs), Lutrelope or Lutrelle (Ferring Pharmaceuticals) and Relisorm (Serono).
 CC -|- SIMILARITY: Belongs to the GnRH family.
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 CC GO; GO:0005625; C:soluble fraction; TAS.
 DR EMBL; X01059; CAA55526; 1;
 DR EMBL; M12578; AAA5916; 1;
 DR EMBL; X15215; CAA33285; 1;
 DR PIR; S05308; PRRHUG;
 DR Genw; HGNC:449; GNRH1.
 DR MIM; 152760; -.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005183; P:luteinizing hormone releasing factor activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
 DR InterPro; IPR002012; Gnrh.
 DR PFam; PF00446; GNRH; 1.
 DR PRINTS; PR01541; GONADOLIBRNT.
 DR PROSITE; PS00473; GNRH; 1.
 DR KW Clearance on pair of basic residues; Hormone; Amidation; Hypothalamus; Placenta; Pharmaceutical; Signal; Polymorphism; Pyrrolidone carboxylic acid.
 KW SIGNAL; 1; 23
 FT CHAIN; 24; 92
 FT PEPTIDE; 24; 33
 FT ACT_SITE; 26; 26
 FT

[3] ACTIVITY.
 PYRROLIDONE CARBOXYLIC ACID.
 AMIDATION (G-34 PROVIDE AMIDE GROUP).
 W -> S (in dbSNP:6105).
 /FTID=VAR_013931.
 SQ 30A7221B076FA79 CRC64;

ACTIVITY.
 PYRROLIDONE CARBOXYLIC ACID.
 AMIDATION (G-34 PROVIDE AMIDE GROUP).
 W -> S (in dbSNP:6105).
 /FTID=VAR_013931.
 SQ 30A7221B076FA79 CRC64;

Query Match Score 64; DB 1; Length 92;
 Best Local Similarity 40.0%; Pred. No. 0.2;
 Matches 5; Mismatches 10; Indels 0; Gaps 0;

Query Match Score 25.8%; DB 1; Length 92;
 Best Local Similarity 40.0%; Pred. No. 0.2;
 Matches 5; Mismatches 10; Indels 0; Gaps 0;

QY 2 HWSYGLRPSSGPSSLKLSIEKGV1 26
 Db 25 HWSYGLRPSSGPSSLKLSIEKGV1 49

RESULT 14
 VGLF-MEASI
 ID_VGLF-MEASI
 STANDARD;
 PRT; 529 AA.
 AC P2631; Q83298;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F1].
 DE Fusion glycoprotein F1].
 GN F.
 OS Measles virus (strain IP-3-Ca) (Subacute sclerosing panencephalitis virus).
 OS Virus; ssRNA negative-strand viruses; Mononegavirales;
 OC Pararnyxoviridae; Paramyxovirinae; Morbillivirurs.
 OC NCBI_TaxID=11237;
 RN [1]
 PP SEQUENCE FROM N.A.
 MEDLINE=92263801; PubMed=1585656;
 RX Schmid A.; Spillehofer P.; Cattaneo R.; Baczkó K.; Ter Meulen V.;
 RA Billerter M.A.;
 RA "Subacute sclerosing panencephalitis is typically characterized by alterations in the fusion protein cytoplasmic domain of the persisting measles virus";
 RT Virchow 188.910-915(1992).
 RT RL -|- FUNCTION: This Protein directs fusion of viral and cellular membranes.
 CC -|- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2 LINKED BY A DISULFIDE BOND.
 CC -|- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC DR EMBL; X16566; CAA34567; 1; -
 CC DR EMBL; X15566; CAA34568; 1; ALT_INIT.
 CC DR HSSP; P04849; ISVP.
 CC DR InterPro; IPR00077; Fusion_gly.
 DR Glycoprotein; Fusion_protein; Transmembrane; Envelope protein; Signal.
 DR Pfam; PF00523; fusion_gly; 1.
 DR FT CHAIN; 1; 27
 DR FT CHAIN; 2; 27
 DR FT CHAIN; 3; 27
 DR FT CHAIN; 4; 27
 DR FT TRANSMEM; 5; 116
 DR FT DOMAIN; 6; 140
 DR FT TRANSMEM; 7; 498
 DR FT DOMAIN; 8; 519
 DR FT DOMAIN; 9; 529
 DR FT DOMAIN; 10; 518
 DR FT DOMAIN; 11; 529
 DR FT DOMAIN; 12; 198
 DR FT DISULFID; 13; 71
 DR FT CARBOHYD; 14; 32
 DR FT CARBOHYD; 15; 64
 DR FT CARBOHYD; 16; 64
 DR FT CARBOHYD; 17; 70
 DR FT CARBOHYD; 18; 70

SQ SEQUENCE 529 AA; 57331 MW; AE987BC9F07E9AA9 CRC64;
 Query Match Score 64; DB 1; Length 529;
 Best Local Similarity 93.3%; Pred. No. 1.4;
 Matches 14; Conservative 0; N mismatches 1; Indels 0; Gaps 0;
 CC
 CY 19 LSEIKEVIVHRLEGV 33
 Db 291 LSEIKEVIVHRLEGV 305

RESULT 15

GONI_HAPBU STANDARD PRT; 94 AA.
 ID GO:0031387; P51978; OS=Homo sapiens (Re: 34, Created)
 AC P01541; GO:0005576; P00446; GO:000513; P00725; P0002012; DR InterPro; IPR004079; Gonadotropin.
 DT 30-MAY-2000 (Re: 31, Last sequence update)
 DT 10-OCT-2003 (Re: 42, Last annotation update)
 DT Progadotropin precursor [Contains: Gonadotropin-releasing hormone (LHRH) I] (LHRH I); Gonadotropin-releasing hormone I (GnRH-1).
 DS hormone releasing hormone I (LHRH I) (LHRH I); GnRH-associated peptide I.
 CN GNRH1
 OS Haplochromis burtoni (Burton's mouthbrooder).
 OC Bivalvia; Monotocardia; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidei;
 OC Cichlidae; Astatotilapia.
 NCBI_TaxID=8153;

DN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95396799; PubMed=1667296;
 RA White S.A., Kasten T.L., Bond C.T., Adelman J.P., Fernald R.D.;
 RT "Three Gondotropin-releasing hormone genes in one organism suggest novel roles for an ancient Peptide."
 RR Proc. Natl. Acad. Sci. U.S.A. 92:8363-8367(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99061842; PubMed=9843638;
 RA White R.B., Fernald R.D.;
 RA "Ontogeny of Gondotropin-releasing hormone (GnRH) gene expression reveals a distinct origin for GnRH-containing neurons in the midbrain.";
 RL Gen. Comp. Endocrinol. 112:322-329(1998).
 RN [3]
 RP SEQUENCE OF 23-32, AND MASS SPECTROMETRY.
 RC TISSUE=Pituitary;
 RX MEDLINE=95372591; PubMed=1644702;
 RA Powell J.F.F., Fischer W.H., Park M., Craig A.G., Rivier J.E.,
 RA Sherwood N.M.;
 RT "Primary structure of solitary form of gondotropin-releasing hormone (GnRH) in cichlid pituitary; three forms of GnRH in brain of cichlid and pumpkinseed fish."
 RL Regul. Pept. 57:43-53(1995).
 CC -1- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS. MAY BE RESPONSIBLE FOR THE REGULATION OF THE HYPOTHALAMIC-PITUITARY-GONADAL AXIS.
 CC -1- CELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN PREOPTIC NEURONS AND IS TRANSPORTED TO THE PITUITARY IN THE PREOPTIC-HYPOPHYSEAL AXONS.
 CC -1- SIMILARITY: Belongs to the GnRH family.

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CC DR EMBL; U31865; AAC5969-1;
 CC EMBL; AF076561; AAC27716.1; -.

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OM protein - Protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 46:4514 Seconds
 (without alignments)
 319.245 Million cell updates/sec

Title: US-09-848-834A-17

Perfect score: 248
 Sequence: 1 XHWSYGLRPGSSPSLKLIS.....HRLEGVEGPSLHNSYGLRFX 47

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 Summaries

Database : SPREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriaph:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	72.5	29.2	87	13	Q9Y126	Oryzopsis aurata
2	72	29.0	534	12	Q04243	measles vir
3	72	29.0	537	12	Q04242	measles vir
4	72	29.0	545	12	Q9PXA4	Oryxoa4 measles vir
5	72	29.0	546	12	Q9IWA5	Oryzopsis rinderepest
6	72	29.0	550	12	P90331	measles vir
7	72	29.0	550	12	Q9QEXO	Oryzopsis meadles vir
8	72	29.0	550	12	Q9QEW9	Oryzopsis meadles vir
9	72	29.0	550	12	P90330	measles vir
10	72	29.0	550	12	Q9QEW7	Oryzopsis meadles vir
11	72	29.0	550	12	Q9WMK4	Oryzopsis meadles vir
12	72	29.0	550	12	Q8V495	Oryzopsis meadles vir
13	72	29.0	550	12	Q8V049	Oryzopsis meadles vir
14	72	29.0	550	12	Q9YJ94	Oryzopsis meadles vir
15	72	29.0	550	12	Q9QEX1	Oryzopsis meadles vir
16	72	29.0	550	12	Q9QEW8	Oryzopsis meadles vir

SEQUENCE FROM N.A.

RC TISSUE-Ovary;

CC	-!- SIMILARITY: BELONGS TO THE GNRH FAMILY.
DR	ENBL: AF04601; AAD04271; -
DR	GO: GO-0005576; C:extracellular; IBA.
DR	GO: GO-0005183; F:luteinizing hormone-releasing factor activity; IBA.
DR	GO: GO-0007255; P:development; IBA.
DR	InterPro: IPR00012; GnrH
DR	PFAM: PF00466; GnrH; 1.
DR	PRINTS: PRO1541; GONADOLIBRNI.
DR	PROSITE: PS00473; GNRH; 1.
KW	Amidation; Hormone.
FT	NON_TER 1
FT	NON_TER 87
FT	87 AA;
SQ	SEQUENCE 87 AA;
SQ	9871 MW;
Query	Match Score 72.5;
Best	Local Similarity Length 87;
	Pred. No. 0.12;

[1] SEQUENCE FROM N.A.

RP STRAIN=K.

RC MEDLINE=1014265; PubMed=11186456;

RA Aianov P.K., Sminnev A.G., Baborodova S.V., Starov S.K., Drygin V.V., Gusev "Primary structure of the F-gene from Rinderpest virus strain K.";

RA Mol. Gen. Mikrobiol. Virusol. 4:29-33 (2000).

[2] SEQUENCE FROM N.A.

RC STRAIN=K;

RA Aianov P.K., Sminnev A.G., Bezborodova S.V., Starov S.K., Drygin V.V., Gusev A.A.;

RA Submitted (MAY 2001) to the EMBL/GenBank/DBJ databases.

DR FIR; PQ0866; PQ0866.

DR FIR; PQ0867; PQ0867.

DR FIR; PQ0873; PQ0873.

DR GO; GO:0019039; P:viral-cell fusion molecule activity; IEA.

DR GO; GO:006948; P:viral-induced cell-cell fusion; IEA.

DR InterPro; IPR000776; Fusion_gly.

DR Pfam; PF00523; fusion_gly; 1.

SQ SEQUENCE 546 AA; 58572 MW; 449B2B2DD7405F0B CRC64;

Query Match 29.0%; Score 72; DB 12; Length 546;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LSEIKGVIVRLEGV 33

Db 284 LSEIKGVIVRLEGV 298

RESULT 6

ID P90331 PRELIMINARY; PRT; 550 AA.

AC P90331_03; Created)

DT 01-MAY-1997 (TRMBLrel. 03, Last sequence update)

DT 01-MAY-1997 (TRMBLrel. 03, Last sequence update)

DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)

DE Fusion protein.

GN F.

OS Measles virus.

CC ssRNA negative-strand viruses; Mononegavirales;

Parvoviridae; Paramyxovirinae; Morbillivirus.

[1] SEQUENCE FROM N.A.

RP STRAIN=NAGAHATA.

RA Sheng J., Watanabe M., Ueda S.;

RA "Selection of a neurotropic variant of measles virus";

RA Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

[2] SEQUENCE FROM N.A.

RC STRAIN=NAGAHATA.

RA Sheng J., Nakanishi M., Watanabe M., Ueda S.;

RA "An amino acid alteration of F protein responsible for the enhanced fusogenicity of measles virus";

RA Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

[3] SEQUENCE FROM N.A.

RC STRAIN=NAGAHATA.

RA Ning X., Ayata M., Morimoto K., Ito N., Shingai M., Kimura M., Ogura H.;

RA "Nucleotide sequences of the fusion protein gene of subacute sclerosing panencephalitis viruses; deduced amino acid sequences showed the cytoplasmic domain highly mutated -truncated, elongated or predicted secondary structure changed."

RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF179432; AAF026971.1; -.

DR PIR; P00376; P0376.

DR HSSP; P04849; ISVP.

DR GO; GO:0019039; P:viral-cell fusion molecule activity; IEA.

DR GO; GO:006948; P:viral-induced cell-cell fusion; IEA.

DR InterPro; IPR000776; Fusion_gly.

DR Pfam; PF00523; fusion_gly; 1.

SQ SEQUENCE 550 AA; 59504 MW; 2AA969D37FA5CA17 CRC64;

Query Match 29.0%; Score 72; DB 12; Length 550;

Best Local Similarity 100.0%; Pred. No. 1.2;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LSEIKGVIVRLEGV 33

Db 288 LSEIKGVIVRLEGV 302

RESULT 8

ID Q9QEW9 PRELIMINARY; PRT; 550 AA.

AC Q9QEW9_13; Created)

DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)

DE Fusion protein.

OS Measles virus.

CC ssRNA negative-strand viruses; Mononegavirales;

Parvoviridae; Paramyxovirinae; Morbillivirus.

[1] SEQUENCE FROM N.A.

RP STRAIN=OSA-2.

RC D63926; BA09958.1; -.

DR EMBL; AF179431; AAF02696.1; -.

DR PIR; P00376; P0376.

DR HSSP; P04849; ISVP.

DR SEQUENCE FROM N.A.

RC Ning X., Ayata M., Morimoto K., Ito N., Shingai M., Kimura M., Ogura H.;

RT "Nucleotide sequences of the fusion protein gene of subacute

RT scleroing panencephalitis viruses; deduced amino acid sequences
 RT showed the cytoplasmic domain highly mutated --truncated, elongated or
 RT predicted secondary structure changed.";
 RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RU EMBL; API:9436; AP02701.1.; -.
 DR PIR; P00376; PQ0376.
 DR HSSP; P04849; ISVP.
 RC GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
 DR GO; GO:0006948; F:viral-induced cell-cell fusion; IEA.
 DR InterPro; IPR000776; Fusion_Gly; 1.
 DR Pfam; PF00523; fusion_GLY; 1.
 SQ SEQUENCE 550 AA; 59405 MW; QAE6DFC5DD22BBA CRC64;

Query Match Score 72; DB 12; Length 550;
 Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LSEIKGVIVHRLGGV 33
 Db 288 LSEIKGVIVHRLGGV 302

RESULT 9

P90330 PRELIMINARY; PRT; 550 AA.

AC P90330; 03. Created)

DT 01-MAY-1997 (TREMBLrel. 03. Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25. Last annotation update)

DB Fusion protein.

GN F.

OS Measles virus.

OC Paramyxoviridae; Paromyxovirinae; Mononegavirales;

NCBI_TaxID=11234; OX

RN Q9WKK4; PRELIMINARY;

RP 09WKK4; PRELIMINARY;

ID 09WKK4; PRELIMINARY;

AC Q9WKK4; PRELIMINARY;

RC 01-NOV-1999 (TREMBLrel. 12. Created)

RA DT 01-NOV-1999 (TREMBLrel. 12. Last sequence update)

RT DT 01-OCT-2003 (TREMBLrel. 25. Last annotation update)

RL DR Fusion protein.

GN F.

OS Measles virus.

OC Paramyxoviridae; Paromyxovirinae; Mononegavirales;

NCBI_TaxID=11234; OX

RN Q9WKK4; PRELIMINARY; PubMed=10400788;

RP RA Johnston I.C.; Ter Mulen V.; Schneider-Schaubies J.,

RA Schaeider-Schaubies S.;

RA "A recombinant measles vaccine virus expressing wild-type

RT glycoproteins : consequences for viral spread and cell tropism.";

RL RL Virol. 13:6903-6915(1999).

DR DR EMBL; AJ133108; CAB38075.1.; -.

DR DR PIR; PQ0376; PQ0376.

DR DR HSSP; P04849; ISVP.

DR DR GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.

DR DR GO; GO:0006948; F:viral-induced cell-cell fusion; IEA.

DR DR InterPro; IPR000776; Fusion_Gly; 1.

DR DR Pfam; PF00523; fusion_GLY; 1.

DR DR Sequence 550 AA; 59500 MW; 8255499968BSB862 CRC64;

SQ Query Match Score 72; DB 12; Length 550;

Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LSEIKGVIVHRLGGV 33
 Db 288 LSEIKGVIVHRLGGV 302

RESULT 10

Q9QEW7 PRELIMINARY; PRT; 550 AA.

ID Q9QEW7; PRELIMINARY; 13. Created)

AC DT 01-MAY-2000 (TREMBLrel. 13. Last sequence update)

RC DT 01-OCT-2003 (TREMBLrel. 25. Last annotation update)

OS Measles virus.

OC Paramyxoviridae; Paromyxovirinae; Mononegavirales;

NCBI_TaxID=11234; OX

RN Q9QEW7; PRELIMINARY; PubMed=10400788;

RP RA Johnston I.C.; Ter Mulen V.; Schneider-Schaubies J.,

RA Schaeider-Schaubies S.;

RA "A recombinant measles vaccine virus expressing wild-type

RT glycoproteins : consequences for viral spread and cell tropism.";

RL RL Virol. 13:6903-6915(1999).

DR DR EMBL; AJ133108; CAB38075.1.; -.

DR DR PIR; PQ0376; PQ0376.

DR DR HSSP; P04849; ISVP.

DR DR GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.

DR DR GO; GO:0006948; F:viral-induced cell-cell fusion; IEA.

DR DR InterPro; IPR000776; Fusion_Gly; 1.

DR DR Pfam; PF00523; fusion_GLY; 1.

DR DR Sequence 550 AA; 59500 MW; 8255499968BSB862 CRC64;

SQ Query Match Score 72; DB 12; Length 550;

Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LSEIKGVIVHRLGGV 33
 Db 288 LSEIKGVIVHRLGGV 302

RESULT 12			
O89495	PRELIMINARY;	PRT;	550 AA.
AC Q89495;			
DT 01-NOV-1996 (TREMBLrel. 01, Created)			
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE Fusion protein.			
GN F.			
OS Measles virus.			
OC Virus, ssRNA, negative-strand viruses; Mononegavirales;			
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.			
OX NCBI_TaxID=11234;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=92230209; PubMed=15665658;			
RX Rota J.S., Hummel K.B., Rota P.A., Bellini W.J.; "Genetic variability of the glycoprotein genes of current wild-type measles isolates," J. Virology 188:1135-1142 (1992).			
RL DR EMBL; MB1903; AAA46422; 1;			
RL DR EMBL; MB1901; AAA46421; 1;			
RL DR P00376; PQ0376.			
DR HSSP; P04849; 1SVF.			
DR GO; GO_0019039; P:viral-cell fusion molecule activity; IEA.			
DR GO; GO_0006948; P:viral-induced cell-cell fusion; IEA.			
DR InterPro; IPR000776; Fusion_gly.			
DR Pfam; PF00533; fusion_gly; 1.			
SQ SEQUENCE 550 AA; 59564 MW; A78EEC9CD6268558 CRC64;			
Query Match * 29.0%; Score 72; DB 12; Length 550; Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 15; Conservative 0; Indels 0; Gaps 0; Gaps 0;			
Db 19 LSEIKGVIVHRLLEGV 33			
Db 288 LSPIKGVIVHRLLEGV 302			
RESULT 13			
O8V049	PRELIMINARY;	PRT;	550 AA.
AC Q8V049;			
DT 01-MAR-2002 (TREMBLrel. 20, Created)			
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE Fusion protein.			
GN F.			
OS Measles virus.			
OC Virus, ssRNA, negative-strand viruses; Mononegavirales;			
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.			
OX NCBI_TaxID=11234;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=9954;			
RC MEDLINE=2163526; PubMed=11773423;			
RA Watu Koumou D., Wild T.F.; "Adaptation of wild-type measles virus to tissue culture.", J. Virol. 76:1505-1509(2002).			
RT DR EMBL; AV059312; AAL29688; 1; -.			
DR PIR; PQ0376; PQ0376.			
DR GO; GO_0019039; P:viral-cell fusion molecule activity; IEA.			
DR GO; GO_0006948; P:viral-induced cell-cell fusion; IEA.			
DR InterPro; IPR000776; Fusion_gly.			
DR Pfam; PF00533; fusion_gly; 1.			
SQ SEQUENCE 550 AA; 9A7ABA99E1DABE9 CRC64;			
Query Match * 29.0%; Score 72; DB 12; Length 550; Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 15; Conservative 0; Indels 0; Gaps 0; Gaps 0;			
Db 19 LSEIKGVIVHRLLEGV 33			
Db 288 LSPIKGVIVHRLLEGV 302			
RESULT 14			
Q9J94	PRELIMINARY;	PRT;	550 AA.
AC Q9J94;			
DT 01-MAY-1999 (TREMBLrel. 10, Created)			
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE Fusion protein.			
OS Measles virus.			
OC Viruses; ssRNA, negative-strand viruses; Mononegavirales;			
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.			
OX NCBI_TaxID=11234;			
RP SEQUENCE FROM N.A.			
RC STRAIN=Masubako;			
RC Ning X., Ayata M., Morimoto K., Ito N., Shingai M., Kimura M., Obara H.;			
RC "Nucleotide sequences of the fusion protein gene of subacute sclerosing panencephalitis viruses: deduced amino acid sequences showed the cytoplasmic domain highly mutated --truncated, elongated or predicted secondary structure changed"; Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.			
DR PIR; AF179410; AF026951; -.			
DR HSSP; P04849; 1SVF.			
DR GO; GO_0019039; P:viral-cell fusion molecule activity; IEA.			
DR GO; GO_0006948; P:viral-induced cell-cell fusion; IEA.			
DR InterPro; IPR000776; Fusion_gly.			
DR Pfam; PF00533; fusion_gly; 1.			
SQ SEQUENCE 550 AA; 9A7ABA99E1DABE9 CRC64;			
Query Match * 29.0%; Score 72; DB 12; Length 550; Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 15; Conservative 0; Indels 0; Gaps 0; Gaps 0;			
Db 19 LSEIKGVIVHRLLEGV 33			
Db 288 LSPIKGVIVHRLLEGV 302			

	SQ	SEQUENCE	550 AA:	59559 MW;	6098E02A7E59E54 CRC64;	Query Match	29.0%;	Score 72;	DB 12;	Length 55	
	Qy	Best Local Similarity	100.0%;	Pred. No.	1..2;	Matches	15;	Conservative	0;	Mismatches	0;
	Db	19	LSEBIKGIVVHRLLEGY			19	LSEBIKGIVVHRLLEGY	33			
	Db	288	LSEBIKGIVVHRLLEGY			288	LSEBIKGIVVHRLLEGY	302			

Search completed: March 10, 2004, 09:25:38
Job time : 46.4514 secs

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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:48 ; Search time 70.7743 Seconds
 (without alignments)
 187.635 Million cell updates/sec

Title: US-09-848-834A-17
 Perfect score: 248
 Sequence: 1 XHWSYGLRPSSSPSILKLS.....HRLEGVEGPSLHWWSYGLRXP 47

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_29Jun04:
 1: GeneseqP1900s:
 2: GeneseqP1900s:
 3: GeneseqP2000s:
 4: GeneseqP2001s:
 5: GeneseqP2002s:
 6: GeneseqP2003as:
 7: GeneseqP2003bs:
 8: GeneseqP2004s:
 %

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution:

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	246	99.2	47	AAU11428	Aau11428 Synthetic
2	246	69.8	34	AAU11424	Aau11424 Synthetic
3	159	64.1	31	AAU11420	Aau11420 Synthetic
4	147.5	59.5	46	AAU11430	Aau11430 Synthetic
5	144	58.1	51	AAU11431	Aau11431 Synthetic
6	141.5	57.1	50	AAU11429	Aau11429 Synthetic
7	117	47.2	42	AAU62705	Aar62705 LHRH-cont
8	117	47.2	42	AAU62708	Aar62708 LHRH-cont
9	116	46.8	27	AAU62707	Aar62707 LHRH-cont
10	116	46.8	27	AAU68567	Aay68567 Peptide i
11	116	46.8	27	AAU91156	Aay91156 MVF Th ep
12	116	46.8	45	AAU62721	Aar62721 LHRH-cont
13	116	46.8	45	ADD8949	Add8949 LHRH Pept
14	113	45.6	27	AAV91163	Aay91163 Modified
15	110	44.4	31	AAV91175	Aay91175 Modified
16	108	43.5	27	AAV91161	Aay91161 Modified
17	108	43.5	27	AAV91167	Aay91167 Modified
18	108	43.5	45	AAU68573	Aay68573 Peptide i
19	108	43.5	45	AAV91165	Aay91165 Modified
20	107	43.1	31	AAV91179	Aay91179 Modified
21	106	42.7	28	AAV91158	Aay91158 Synthetic
22	106	42.7	40	AAW79581	Aaw79581 Measles v
23	106	42.7	40	AAV79986	Aay79986 Measles v
24	106	42.7	40	ADA5172	Ada25172 Chimeric
25	106	42.7	40	ADCB89661	Adc89661 H. influe

ALIGNMENTS

RESULT 1
 ID AAU11428 standard; peptide: 47 AA.

AC AAU11428;

XX
 DT 12-MAR-2002
 XX

DE Synthetic immunogen Peptide 9.

XX Gonadotrophin releasing hormone; GnRH; synthetic immunogen;
 KW luteinising hormone releasing hormone; LHRH; contraceptive;
 KW promiscuous helper T-cell peptide epitope; immunohormone peptide epitope;
 KW breast cancer; uterine cancer; gynaecological cancer; endometriosis;
 KW uterine fibroid; benign prostatic hypertrophy; prostate cancer.
 XX Plasmodium falciparum.
 OS Mammalia.
 OS Chimeric.
 OS

Location/Qualifiers

1. .10 "Gonadotrophin releasing hormone epitope (1...10 aa)"
 1 /label= OTHER /note= "Pyro-glutamic acid or 5-oxo Proline"
 1 /label= OTHER /note= "Spacer peptide"
 17. .34 /note= "Malaria CSP protein (288-302 aa)"
 35. .38 /note= "Spacer peptide"
 39. .47 /note= "Gonadotrophin releasing hormone epitope (2-10 aa)"
 47 /note= "Amidated glycine or glycynamide"
 XX
 FT Key Peptide
 FT Peptide
 FT Misc-difference
 FT Peptide
 XX
 PN WO2001B5763-A2.

15-NOV-2001.

04-MAY-2001; 2001WO-US014363.

05-MAY-2000; 2000US-02238P.

PA (APHT-) APHTON CORP.
 XX
 PI Grimes S, Michaeli D, Stevens VC;
 XX
 WPI; 2002-049440/06.
 DR XX
 PT Novel synthetic immunogen for inducing immune response against
 PT gonadotropin releasing hormone, comprises fusion peptide having
 PT promiscuous helper T-cell peptide epitope and immunomimetic peptide epitope
 PT or its analog.
 XX
 PS Claim 11; Page 11; 43PP; English.
 CC The invention relates to a synthetic immunogen for inducing specific
 CC antibodies against gonadotropin releasing hormone (GnRH also known as
 CC luteinising hormone releasing hormone, LHRH) comprising a fusion peptide
 CC which comprises a promiscuous helper T-cell peptide epitope and
 CC immunomimetic peptide epitope or its analogue. The synthetic immunogen is
 CC useful inducing an immune response against GnRH in an animal subject, and
 CC such is useful as a contraceptive and in the treatment of diseases
 CC such as cancer (of the breast, uterus and other gynaecological cancer),
 CC endometriosis, uterine fibroids, benign prostatic hypertrophy and
 CC prostate cancer. The immunogen is effective in eliciting high and
 CC specific anti-GnRH antibody titres. The present sequence is a synthetic
 CC immunogen of the invention
 XX Sequence 47 AA;

Query Match 99.2%; Score 246; DB 5; Length 47;
 Best Local Similarity 100.0%; Pred. No. 4_7e-25;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 HWSYGLRPSSGPSPSLKLSEIKGVTVHLRLEGVEGPSLHWSYGLRP 46
 2 HWSYGLRPSSGPSPSLKLSEIKGVTVHLRLEGVEGPSLHWSYGLRP 46

RESULT 2
 ID AAU11424 standard; peptide: 34 AA.
 XX
 AC AAU11424;
 XX
 DT 12-MAR-2002 (first entry)
 DE Synthetic immunogen Peptide 5.
 XX
 Gonadotrophin releasing hormone; GnRH; synthetic immunogen;
 KW luteinising hormone releasing hormone; LHRH; contraceptive;
 KW promiscuous helper T-cell peptide epitope; immunomimetic peptide epitope;
 KW breast cancer; uterine cancer; gynaecological cancer; endometriosis;
 KW uterine fibroid; benign prostatic hypertrophy; prostate cancer.
 XX
 Measles virus.
 OS Mammalia.
 OS Chimeric.
 XX
 Key Location/Qualifiers
 PT Peptide 1..10 /note= "Gonadotrophin releasing hormone epitope"
 PT Misc-difference 1 /label= OTHER /note= "Other= Pyro-glutamic acid or 5-oxo proline"
 PT Peptide 11..16 /note= "Spacer peptide"
 PT Peptide 17..34 /note= "Measles virus fusion protein F epitope"
 PT Peptide 18..31 /note= "Gonadotrophin releasing hormone epitope"
 XX
 WO200185763-A2.
 XX
 PD 15-NOV-2001.

PP 04-MAY-2001; 2001WO-US014363.
 XX
 PR 05-MAY-2000; 2000US-0202328P.
 XX
 (APHT-) APHTON CORP.
 XX
 PI Grimes S, Michaeli D, Stevens VC;
 XX
 WPI; 2002-049440/06.
 DR XX
 PT Novel synthetic immunogen for inducing immune response against
 PT gonadotropin releasing hormone, comprises fusion peptide having
 PT promiscuous helper T-cell peptide epitope and immunomimetic peptide epitope
 PT or its analog.
 XX
 PS Claim 11; Page 9; 43PP; English.
 CC The invention relates to a synthetic immunogen for inducing specific
 CC antibodies against gonadotropin releasing hormone (GnRH also known as
 CC luteinising hormone releasing hormone, LHRH) comprising a fusion peptide
 CC which comprises a promiscuous helper T-cell peptide epitope and
 CC immunomimetic peptide epitope or its analogue. The synthetic immunogen is
 CC useful inducing an immune response against GnRH in an animal subject, and
 CC such is useful as a contraceptive and in the treatment of diseases
 CC such as cancer (of the breast, uterus and other gynaecological cancer),
 CC endometriosis, uterine fibroids, benign prostatic hypertrophy and
 CC prostate cancer. The immunogen is effective in eliciting high and
 CC specific anti-GnRH antibody titres. The present sequence is a synthetic
 CC immunogen of the invention
 XX Sequence 34 AA;

Query Match 69.8%; Score 173; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.5e-15;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HWSYGLRPSSGPSPSLKLSEIKGVTVHLRLEGVE 34
 Db 2 HWSYGLRPSSGPSPSLKLSEIKGVTVHLRLEGVE 34

RESULT 3
 AAU11420 standard; peptide: 31 AA.
 ID AAU11420
 XX
 AC AAU11420;
 XX
 DT 12-MAR-2002 (first entry)
 DE Synthetic immunogen Peptide 1.
 XX
 Gonadotrophin releasing hormone; GnRH; synthetic immunogen;
 KW luteinising hormone releasing hormone; LHRH; contraceptive;
 KW promiscuous helper T-cell peptide epitope; immunomimetic peptide epitope;
 KW breast cancer; uterine cancer; gynaecological cancer; endometriosis;
 KW uterine fibroid; benign prostatic hypertrophy; prostate cancer.
 XX
 Measles virus.
 OS Mammalia.
 OS Chimeric.
 XX
 Key Location/Qualifiers
 PT Peptide 1..10 /note= "Gonadotrophin releasing hormone epitope"
 PT Misc-difference 1 /label= OTHER /note= "Other= Pyro-glutamic acid or 5-oxo proline"
 PT Peptide 11..16 /note= "Spacer peptide"
 PT Peptide 17..34 /note= "Measles virus fusion protein F epitope"
 PT Peptide 18..31 /note= "Gonadotrophin releasing hormone epitope"
 PT Modified-site 31 /note= "Amidated glycine or glycaminide"
 PT
 PN WO200185763-A2.

PP 1..18 /note= "Measles virus fusion protein F epitope"
 PT Peptide 19..22 /note= "Spacer peptide"
 PT Peptide 23..31 /note= "Gonadotrophin releasing hormone epitope"
 PT Modified-site 31 /note= "Amidated glycine or glycaminide"
 PN WO200185763-A2.

XX /note= "Spacer peptide"
 XX 17. .31 "Tetanus toxoid (830-844 aa)"
 XX /note= "Spacer peptide"
 XX 32. .37 "Spacer peptide"
 XX /note= "Spacer peptide"
 XX 38. .46 "Gonadotrophin releasing hormone epitope (2-10
 AA)"
 XX /note= "Amidated Glycine or glycaminide"
 PI FT Peptide
 PI FT Peptide
 PR FT Peptide
 PR FT Peptide
 PA FT Modified-site
 PA FT Modified-site
 PI FT Peptide
 XX PN WO200185763-A2.
 DR XX 15-NOV-2001.
 PT XX 15-NOV-2001.
 PR XX 04-MAY-2001; 2001WO-US014363.
 PT XX 04-MAY-2001; 2001WO-US014363.
 PS XX 05-MAY-2000; 2000US-0202328P.
 PA XX (AEPHT-) APITON CORP.
 PI Grimes S, Michaeli D, Stevens VC;
 XX WPT; 2002-049440/06.
 XX Novel synthetic immunogen for inducing immune response against
 PT gonadotropin releasing hormone, comprises fusion peptide having
 PR promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
 PT or its analog.
 PS XX Claim 11; Page 7; 43PP; English.
 CC The invention relates to a synthetic immunogen for inducing specific
 CC antibodies against gonadotropin releasing hormone (GnRH) also known as
 CC luteinising hormone releasing hormone, (LHRH) comprising a fusion peptide
 CC which comprises a promiscuous helper T-cell peptide epitope and
 CC immunomimic peptide epitope or its analogue. The synthetic immunogen is
 CC useful inducing an immune response against GnRH in an animal subject, and
 CC such as useful as a contraceptive and in the treatment of diseases
 CC such as cancer (of the breast, uterus and other gynaecological cancer),
 CC endometriosis, uterine fibroids, benign prostatic hypertrophy and
 CC prostate cancer. The immunogen is effective in eliciting high and
 CC specific anti-GnRH antibody titres. The present sequence is a synthetic
 CC immunogen of the invention.
 XX Sequence 31 AA;
 SQ Query Match 64.1%; Score 159; DB 5; Length 31;
 Best Local Similarity 100.0%; Pred. No. 9.3e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 17 KLLSEIKGIVVHLLEGTEGPSLHWSYGLRP 46
 Db 1 KLLSEIKGIVVHLLEGTEGPSLHWSYGLRP 30
 RESULT 4
 AAU11430
 ID AAU11430 standard; peptide; 46 AA.
 XX AAU11430;
 AC AAU11430;
 XX DT 12-MAR-2002 (first entry)
 DE Synthetic immunogen Peptide 11.
 XX Gonadotrophin releasing hormone; GnRH; synthetic immunogen;
 KW luteinising hormone releasing hormone; LHRH; contraceptive;
 KW promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
 KW breast cancer; uterine cancer; gynaecological cancer; endometriosis;
 KW uterine fibroid; benign prostatic hypertrophy; prostate cancer.
 XX Clostridium tetani.
 OS Mammalia.
 OS Synthetic.
 OS Chimeric.
 XX Key Location/Qualifiers
 PH 1..10
 PT 1..10 "Gonadotrophin releasing hormone epitope (1. .10
 PT aa)"
 PT Misc-difference 1
 PT /label= OTHER
 PT /note= "Other= Pyro-glutamic acid or 5-oxo proline"
 PT 11. .16
 Peptide OS Plasmodium falciparum.

OS Mammalia.
 OS Synthetic.
 XX Chimeric.
 Key Peptide
 PT Peptide 1..10
 /note= "Gonadotrophin releasing hormone epitope (1..10
 aa)"
 PT Misc-difference 1
 /label= OTHER
 /note= "Other= Pyro-Glutamic acid or 5-oxo proline"
 PT Peptide 11..16
 /note= "Spacer peptide"
 PT Peptide 17..36
 /note= "Malaria CSP Protein (378-396 aa)"
 PT Peptide 37..42
 /note= "Spacer peptide"
 PT Peptide 43..51
 /note= "Gonadotrophin releasing hormone epitope (2-10
 aa)"
 PT Modified-site 51
 /note= "Amidated glycine or glycynamide"
 XX WO200185763-A2.
 PN PD 15-NOV-2001.
 XX PP 04-MAY-2001; 2001WO-US014363.
 XX PR 05-MAY-2000; 2000US-0202328P.
 PA (APHT-) APHTON CORP.
 PI Grimes S, Michaeli D, Stevens VC;
 XX DR 2002-049440/06.
 XX Novel synthetic immunogen for inducing immune response against
 PT gonadotropin releasing hormone, comprises fusion peptide having
 PT immunomimetic peptide epitope and immunomimetic peptide epitope
 PT or its analog.
 PS Claim 11; Page 12-13; 43PP; English.
 XX The invention relates to a synthetic immunogen for inducing specific
 CC antibodies against gonadotropin releasing hormone (GnRH also known as
 CC luteinising hormone releasing hormone, LHRH) comprising a fusion peptide
 CC which comprises a promiscuous helper T-cell peptide epitope and
 CC immunomimetic peptide epitope or its analogue. The synthetic immunogen is
 CC useful, inducing an immune response against GnRH in an animal subject, and
 CC such as useful as a contraceptive and in the treatment of diseases
 CC such as cancer (of the breast, uterus and other gynaecological cancer),
 CC endometriosis, uterine fibroids, benign prostatic hypertrophy and
 CC prostate cancer. The immunogen is effective in eliciting high and
 CC specific anti-GnRH antibody titres. The present sequence is a synthetic
 CC immunogen of the invention
 XX Sequence 51 AA;
 SQ Query Match Similarity 58.1%; Score 144; DB 5; Length 51;
 Best Local Similarity 57.1%; Pred. No. 1..7e-11; N-matches 8; Gaps 2;
 Matches 28; Conservative 8;
 Oy 2 HWSYGLRPSSGPSSL-KLISBIK--GVIVHLRBLGEVGPSSLHWSYGLRP 46
 Db 2 HWSYGLRPSSGPSSLDEKKIANKMERASSVFNVNSSSGPSSLHWSYGLRP 50
 RESULT 6
 ID AAU11429 standard; Peptide; 50 AA.
 XX AC AAU11429;

XX 12-MAR-2002 (first entry)
 DT XX Synthetic immunogen peptide 10.
 DE XX
 KW Gondotrophin releasing hormone; GnRH; synthetich immunogen;
 KW luteinising hormone releasing hormone; LHRH; contraceptive;
 KW promiscuous helper T-cell peptide epitope; immunomimetic peptide epitope;
 KW breast cancer; uterine cancer; gynaecological cancer; endometriosis;
 KW uterine fibroid; benign prostatic hypertrophy; prostate cancer.
 XX
 OS Clostridium tetani.
 OS Mammalia.
 OS Synthetic.
 OS Chimeric.
 XX
 Key Peptide
 PT Peptide 1..10
 /note= "Gonadotrophin releasing hormone epitope (1..10
 aa)"
 XX Location/Qualifiers
 FH Key
 FT Peptide
 FT Peptide 1..10
 /note= "Gonadotrophin releasing hormone epitope (1..10
 aa)"
 FT Peptide
 FT Peptide 1..16
 /note= "Pyro-glutamic acid or 5-oxo proline"
 FT Misc-difference 1
 FT Peptide
 FT Peptide 11..16
 /note= "Spacer peptide"
 FT Peptide
 FT Peptide 17..37
 /note= "Tetanus toxoid (947-967 aa)"
 FT Peptide
 FT Peptide 38..41
 /note= "Spacer peptide"
 FT Peptide
 FT Peptide 42..50
 /note= "Gonadotrophin releasing hormone epitope (2-10
 aa)"
 FT Modified-site 50
 /note= "Amidated glycine or glycynamide"
 XX WO200185763-A2.
 XX PD 15-NOV-2001.
 XX PP 04-MAY-2001; 2001WO-US014363.
 XX PR 05-MAY-2000; 2000US-0202328P.
 XX PA (APHT-) APHTON CORP.
 XX PI Grimes S, Michaeli D, Stevens VC;
 XX DR 2002-049440/06.
 XX Novel synthetic immunogen for inducing immune response against
 PT gonadotropin releasing hormone, comprises fusion peptide having
 PT immunomimetic peptide epitope and immunomimetic peptide epitope
 PT or its analog.
 PS Claim 11; Page 11; 43PP; English.
 XX The invention relates to a synthetic immunogen for inducing specific
 CC antibodies against gonadotropin releasing hormone (GnRH also known as
 CC luteinising hormone releasing hormone, LHRH) comprising a fusion peptide
 CC which comprises a promiscuous helper T-cell peptide epitope and
 CC immunomimetic peptide epitope or its analogue. The synthetic immunogen is
 CC useful, inducing an immune response against GnRH in an animal subject, and
 CC such as useful as a contraceptive and in the treatment of diseases
 CC such as cancer (of the breast, uterus and other gynaecological cancer),
 CC endometriosis, uterine fibroids, benign prostatic hypertrophy and
 CC prostate cancer. The immunogen is effective in eliciting high and
 CC specific anti-GnRH antibody titres. The present sequence is a synthetic
 CC immunogen of the invention
 XX Sequence 50 AA;
 SQ Query Match Similarity 57.1%; Score 141.5; DB 5; Length 50;
 Best Local Similarity 58.8%; Pred. No. 3..5e-11;
 AC AAU11429;

CC dependent carcinoma, prostatic carcinoma, testicular carcinoma, endometriosis, benign uterine tumours, recurrent functional ovarian cancer, (severe) premenstrual syndrome, or oestrogen-dependent breast cancer, or for induction of infertility. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 42 AA;

Query Match Score 47.2%; Best Local Similarity 82.8%; Length 42; Matches 24; Conservative 1; Mismatches 2; Indels 2; Gaps 1; Qy 1.8 LLSEIKGVIVHRLLEGVEGPSLWVSYGLRP 46 Db 1.5 VLSEIKGVIVARLEGVGEB-HWSYGLRP 41

RESULT 9

AAR62707 standard; peptide: 27 AA.

XX AAR62707; XX DT 25-MAR-2003 (revised) DT 10-SEP-1995 (first entry)

XX LHRH-containing immunogenic peptide.

DE Helper T cell epitope; universal immune stimulator; invasin; hapten; vaccine; LHRH; luteinising hormone releasing hormone; prostate; androgen-dependent carcinoma; antitumour; infertility; measles virus F protein.

OS Synthetic.

FH Key Domain 1..15 note: "measles virus F protein helper T cell epitope"

PT Domain 18..27 note: "LHRH hapten"

FT Domain 1..15 note: "measles virus F protein helper T cell epitope"

PT Domain 18..27 note: "LHRH hapten"

XX WO9425050-A1.

XX PD 10-NOV-1994.

XX PF 28-APR-1994; 94WO-US004832.

XX PR 27-APR-1993; 93US-00057166.

XX PR 14-APR-1994; 94US-00229275.

XX PA (LADD/) LADD A. E.

PA (WANG/) WANG C. Y.

PA (ZAMB/) ZAMB T.

XX PI Ladd AE, Wang CY, Zamb T;

XX DR; 1994-357910/44.

XX PT Immunogenic luteinising hormone releasing hormone peptide(s) - that suppress LHRH activity in males and females.

XX PT Claim 8, 12; Page 86; 213pp; English.

XX CC Synthetic immunogenic peptides are provided in which a universal immune stimulator is linked to a peptide or protein hapten containing B cell and/or cytotoxic T lymphocyte epitopes, giving a product which causes potent immune responses to the coupled peptide or protein. The stimulator consists of (A) a promiscuous helper T cell epitope (Th) which elicits an immune response to the coupled peptide in members of a heterogeneous population expressing diverse HLA phenotypes, and (B) an adjuvant peptide sequence from the invasin protein of Yersinia. Spacer amino acid

CC sequences (e.g. Gly-Gly) can be provided between the invasin and Th domains and between the immune stimulator and hapten components. When the

hapten is LHRH, then optionally the invasin domain can be omitted from the immune stimulator component. The present sequence represents an LHRH-containing, invasin-free immunogenic peptide as above which can be used as a potent vaccine for treating e.g. prostatic hyperplasia, androgen-dependent carcinoma, prostatic carcinoma, testicular carcinoma, endometriosis, benign uterine tumours, recurrent functional ovarian cysts, (severe) premenstrual syndrome or oestrogen-dependent breast cancer, or for induction of infertility. This sequence is particularly preferred. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 27 AA; SO Sequence 27 AA;

Query Match Score 46.8%; Best Local Similarity 85.7%; Pred. No. 3.9e-08; Matches 24; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy 19 LSEIKGVIVHRLLEGVEGPSLWVSYGLRP 46

Db 1 LSEIKGVIVHRLLEGVGEB-HWSYGLRP 26

RESULT 10

AAV68567 ID AAV68567 standard; peptide: 27 AA.

XX AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-MAY-2000 (first entry)

XX Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX DB Peptide immunogen comprising a Th epitope and LHRH target antigen.

XX AC AAV68567;

XX AC AAV68567;

XX DT 05-M

CC immunogens cause induction of a specific immune response to LHRH which is involved in regulation of spermatogenesis, ovulation, oestrus, sexual development and secretion of sex hormones. Provision of a promiscuous T helper epitope (which is functional in genetically diverse subjects) provides optimum immunogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (reversible) contraceptive; control of hormone dependent tumours (cancer of prostate or breast, also endometriosis); to prevent boar taint (and improve meat quality) and for immunocastration.

XX Sequence 27 AA;

Query Match Score 116; DB 3; Length 27;
Best Local Similarity 85.7%; Pred. No. 3.9e-08;
Matches 24; Conservative 0; N mismatches 2; Indels 2; Gaps 1;

QY 19 LSEIKGVIVRLEGVEGGPSLHWSYGLRP 46

DB 1 LSEIKGVIVRLEGVEE-HWSYGLRP 26

RESULT 11
AY91156 ID AY91156 standard; peptide: 27 AA.
XX AAY91156;

XX DT 12-SEP-2003 (revised)
DT 22-MAY-2000 (first entry)

XX MvF Th epitope/LHRH antigenic peptide, SEQ ID NO:36.

Promiscuous T-cell epitope; measles virus F protein; MvF; hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic; Plasmidum falciparum; circumsporozoite; antimarial; CTP; cholestryl ester transport protein; anti-arteriosclerotic.
XX Measles virus.
OS Rattus sp.
OS Chimeric.
XX PN W09966957-A2.
XX PD 29-DEC-1999.
XX PF 21-JUN-1999; 99WO-US013375.
XX PR 20-JUN-1998; 98US-00100412.
XX PA (UNIBI-) UNITED BIOMEDICAL INC.
PI Wang CY;
XX DR 2000-160564/14.

XX New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus.
XX Example 1; Page 77; 129pp; English.
XX The invention relates to novel promiscuous T helper cell epitopes (Th), CC and immunogenic peptides comprising the Th epitopes of the invention CC along with B cell epitopes. The Th epitopes and peptide immunogens CC containing them, are used to induce a T helper cell response, specifically against Plasmidum falciparum, cholestryl ester transport CC protein (CTP) or HIV epitopes, but more generally against any pathogen, CC immunoreactive self-antigen or tumour antigen. The Th epitopes and CC peptide immunogens may be used for prevention and/or treatment of

CC infections (HIV, foot-and-mouth disease or malaria); for cancer CC immunotherapy; for inhibition of the action of luteinising hormone CC releasing hormone (LHRH) for contraception, treatment of hormone- CC dependent cancer, prevention of bear taint in meat, and immunocastration) CC ; for promoting the growth of animals; or for treating allergies or CC arteriosclerosis. Incorporation of a promiscuous Th (functional in CC genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in CC production of antibodies against a target antigen. This can replace carrier CC proteins and pathogen-derived T helper epitopes. Sequence AAY91121 CC represents a promiscuous T helper epitope from the MVF virus F (MVF) CC protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246 CC represent synthetic Th epitopes based on the MVF Th epitope. Sequence CC AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV) CC surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes CC derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242- CC Y91244 are antigenic peptides comprising an LHRH sequence joined to a CC promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide CC used in these LHRH antigenic peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th CC epitope. Somatostatin immunogens may be used to promote growth in CC livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and CC AAY91209-Y91211 are MVF Th epitope/CD4 CDR2 antigenic peptides which may CC be used to prevent HIV infection of T cells. AAY91212 is a modified CC version of a human IgB (immunoglobulin E) CH3 domain, and AAY9013-Y90219 CC are Th epitope/IgE CH3 antigenic peptides which may be used in the CC treatment of allergies. AAY91220 is a peptide derived from foot and mouth CC disease virus (FMDV) VP1 capsid protein and AAY91222 comprise this CC peptide and a Th epitope. AAY91223 is a Plasmidum falciparum CC circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS CC antigen and an MVF Th epitope and may be used in a malaria vaccine. CC AAY91228-Y91231 are CTP-derived peptides and AAY91232-Y91241 are CC immunogens comprising CTP peptide and Th epitope which may be used CC to prevent or treat arteriosclerosis and cardiovascular disease. AAY91248- CC Y91251 and AAY91258-Y91273 are HIV-1 neutralising MVF Th and CC HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 CC vaccine. AAY91198 and AAY91199 are respectively an immunomodulatory CC invasin protein epitope from Yersinia species, and hinge spacer peptide, CC both of which may optionally be used in the antigenic peptides of the CC invention. (Updated on 12-SEP-2003 to standardise OS field)

XX SQ Sequence 27 AA;

Query Match Score 116; DB 3; Length 27;
Best Local Similarity 85.7%; Pred. No. 3.9e-08;
Matches 24; Conservative 0; N mismatches 2; Indels 2; Gaps 1;

QY 19 LSEIKGVIVRLEGVEGGPSLHWSYGLRP 46
Db 1 LSEIKGVIVRLEGVEGGE-HWSYGLRP 26

RESULT 12
AAY91221 ID AAY91221 standard; peptide: 45 AA.
XX AC AAY91221;
XX DT 25-MAR-2003 (revised)
DT 10-SEP-1995 (first entry)
XX DE LHRH-containing immunogenic peptide.
XX KW Helper T cell epitope/universal immune stimulator; invasin; happen;
KW vaccine; LHRH; luteinising hormone releasing hormone; Prostate;
KW androgen-dependent carcinoma; antitumour; infertility;
KW measles virus F protein.
XX Synthetic.
PH Key
FT Domain 1..16 Location/Qualifiers

XX	WO2003068169-A2.
PN	
XX	21-AUG-2003 .
PD	
XX	14-FEB-2003 ; 2003WO-US004711.
PF	
XX	PR 14-FEB-2002 ; 2002US-00076674.
PT	
XX	PR 3-JAN-2003 ; 2003US-00076674.
PT	
XX	PA (UNIBI-) UNITED BIOMEDICAL INC.
PA	
PI	Sokoll KK;
XX	DR WPI; 2003-778890/73.
XX	PR Stabilized immunostimulating complex, useful for vaccination, e.g. against human immune deficiency viruses, comprises cationic peptide immunogen and anionic oligonucleotide.
PT	
XX	PT Claim 17; SEQ ID NO 9; 159pp; English.
PS	
XX	CC The present sequence is that of a synthetic immunogenic peptide derived from human LHRH. This is an example of peptides that can be used in claimed immunostimulatory complexes of the invention that can be used in CC specifically adapted to act as adjuvant and as peptide immunogen CC stabiliser. The complexes comprise a CpG oligonucleotide and a biologically active peptide immunogen. The complex is particulate and can CC efficiently present peptide immunogens to the cells of the immune system CC to produce an immune response. The complexes may be prepared with various ratios of peptides to CpG oligonucleotides to provide different physical CC properties, such as the size of the microparticle. An immunostimulatory CC complex comprising the present LHRH derived peptide can be used in a CC vaccine for prostate cancer.
SQ	Sequence 45 AA;
XX	Query Match Score 46.8%; Score 116; DB 7; Length 45; Best Local Similarity 85.7%; Pred. No. 7.3e-08; Matches 24; Conservative 0; Mismatches -2; Indels 2; Gaps 1
Qy	19 LSRIKGVIVHLRLEGVEGPGSLHWSYGLRP 46
Db	19 LSRIKGVIVHLRLEGVEGPGGE-HWSYGLRP 44
RESULT 14	
AAV91163	Modified Mvv Th epitope/LHRH antigenic peptide, SEQ ID NO:43.
ID AAV91163 standard; Peptide: 27 AA.	
XX	
AC AAV91163;	
XX	
DT 12-SEP-2003 (revised)	
DT 22-MAY-2000 (first entry)	
XX	
DE Modified Mvv Th epitope/LHRH antigenic peptide, SEQ ID NO:43.	
XX	Promiscuous T-cell epitope; measles virus F protein; MVF; B-cell epitope;
KW hepatitis B virus surface antigen; HBV; immunogenic;	
KW luteinizing hormone releasing hormone; LHRH; contraceptive; anticancer;	
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;	
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;	
KW Plasmodium falciparum; circumsporozoite; antimalarial; CEPN1;	
KW cholesteroyl ester transport protein; anti-arteriosclerotic.	
XX	
OS Measles virus.	
OS Rattus sp.	
XX	Chimeric.
PN WO966957-A2.	
XX	
PD 29-DEC-1995.	

PF 21-JUN-1999; 99WO-US013975.
 XX PR 20-JUN-1998; 98US-00100412.
 XX PA (UNIBI-) UNITED BIOMEDICAL INC.
 XI Wang CY;
 XX DR WPI; 2000-160564/14.
 XX PT New artificial T helper cell epitope and derived immunogens with target
 XX antigenic site, for immunization against e.g. malaria, arteriosclerosis
 or human immune deficiency virus.
 XX PS Example 1; Page 80; 129pp;.English.

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesteryl ester transport protein (CETP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of luteinising hormone-releasing hormone (LHRH) for contraception, treatment of hormone-dependent cancer, prevention of boar taint in meat, and immunocastration (for promoting the growth of animals; or for treating allergies or arteriosclerosis). Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antigen. Th can replace carrier proteins and pathogen-derived T helper epitopes. Sequence AAY91121 represents a promiscuous T helper epitope from the measles virus F (MVF) protein and sequences AAY91122-Y91142, AAY91226 and AAY9145-Y91246 represent synthetic Th epitopes based on the MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope. AAY91197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are synthetic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in AAY91208 is a human CD4 CDR2-like domain antigenic site, and AAY9109-Y90211 are MVH Th epitope. AAY91202 is a modified version of HIV infection of T cells. AAY90212 is a modified CS version of human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3 antigenic peptides which may be used in the treatment of allergies. AAY91220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th epitope which may be used in a malaria vaccine. AAY9126-Y91231 represent CETP-derived peptides and AAY9132-Y91241 are immunogens comprising a CETP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247 and AAY9125-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-HIV1 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 27 AA;

Query Match 45.6%; Score 113; DB 3; Length 27;
 Best Local Similarity 82.1%; Pred. No. 9.7e-08;
 Matches 23; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Db 1 LSEIKGVIVHKLEGVGGE - HWSYGLRP 26
 RESULT 15
 ID AAY91175 standard; peptide; 31 AA.
 XX AC AAY91175;
 XX DT 12-SEP-2003 (revised)
 XX DT 22-MAY-2000 (first entry)
 DE Modified MVF Th epitope/LHRH antigenic peptide, SEQ ID NO:55.
 XX KW Promiscuous T-cell epitope; measles virus F protein; MVF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CM receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
 KW cholesteryl ester transport protein; anti-arteriosclerotic.
 XX Measles virus.
 OS Ratius sp.
 OS Chimeric.
 XX PN WO966957-A2.
 XX PD 29-DEC-1999.
 XX PP 21-JUN-1999; 99WO-US013975.
 XX PR 20-JUN-1998; 98US-00100412.
 XX PA (UNIBI-) UNITED BIOMEDICAL INC.
 PI Wang CY;
 DR WPI; 2000-160564/14.
 XX PT New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus.
 XX PS Example 1; Page 84; 129pp; English.
 XX The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesteryl ester transport protein (CETP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of luteinising hormone-protein (LHRH) for contraception, treatment of hormone-dependent cancer, prevention of boar taint in meat, and immunocastration (for promoting the growth of animals; or for treating allergies or arteriosclerosis). Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antigen. Th can replace carrier proteins and pathogen-derived T helper epitopes. Sequence AAY91121 represents a promiscuous T helper epitope from the measles virus F (MVF) protein and sequences AAY91122-Y91142, AAY91226 and AAY9145-Y91246 represent synthetic Th epitopes based on the MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope. AAY91197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are synthetic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in AAY91208 is a human CD4 CDR2-like domain antigenic site, and AAY9109-Y90211 are MVH Th epitope. AAY91202 is a modified version of HIV infection of T cells. AAY90212 is a modified CS version of human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3 antigenic peptides which may be used in the treatment of allergies. AAY91220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th epitope which may be used in a malaria vaccine. AAY9126-Y91231 represent CETP-derived peptides and AAY9132-Y91241 are immunogens comprising a CETP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247 and AAY9125-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-HIV1 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 27 AA;

Query Match 45.6%; Score 113; DB 3; Length 27;
 Best Local Similarity 82.1%; Pred. No. 9.7e-08;
 Matches 23; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

CC Sequence 27 AA;

Query Match 45.6%; Score 113; DB 3; Length 27;
 Best Local Similarity 82.1%; Pred. No. 9.7e-08;
 Matches 23; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

CC 1 LSEIKGVIVHKLEGVGGE - HWSYGLRP 46

used in these LHRH antigenic peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV infection of T cells. AAY90212 is a modified version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3 antigenic peptides which may be used in the treatment of allergies. AAY91220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th epitope and may be used in a malaria vaccine. AAY91226-Y91231 represent CERP-driven peptides and AAY91227-Y91241 are immunogens comprising a CERP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention. (Updated on 12-SEP-2003 to standardise CS field)

Sequence 31 AA:

Query Match	Score	DB	Length	31;
Best Local Similarity	44.4%			
Matches	78.6%	Pred. No.	2.9e-07;	
22;	Conservative	Mismatches	5;	
		Indels	0;	
		Gaps	0;	

Qy 19 LSEIKGVIVTHRLLEGVEGGSILHNSYGLRP 46
 Db 3 LSEIKGVIVTHKLGSVLFGGEHNSYGLRP 30

Search completed: March 10, 2004, 09:12:13
 Job time : 71.7743 secs

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OM protein - protein search, using sw model1

Run on: March 10, 2004, 09:16:59 ; Search time 36.9416 Seconds

(without alignments)
 268.645 Million cell updates/sec

Title: US-09-848-834A-17

Perfect score: 248

Sequence: 1 XWMSYGLRPSSGPSSLKLS.....HRLLEGVEGSPSLHWSYGLRPX 47

Scoring table: BLOSUM62

Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 8097442

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : Published Applications A: *

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17: /cgn2_6/picodata/2/pubpaas/us6_NEW_PUB.pep:*

18: /cgn2_6/picodata/2/pubpaas/us6_PUBCOMB.pep:*

RESULT 1
 US-09-848-834A-17

; Sequence 17, Application US/0948834A

; Patent No. US20076416A1

; GENERAL INFORMATION:

; APPLICANT: Abitron Corporation Peptide Immunogens

; TITLE OF INVENTION: Chimeric Peptide Immunogens

; FILE REFERENCE: 1102865-0047

; CURRENT APPLICATION NUMBER: US/09/848-834A

; PRIORITY FILING DATE: 2001-05-04

; PRIOR APPLICATION NUMBER: 60/202,328

; PRIOR FILING DATE: 2000-05-05

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO: 17

; LENGTH: 47

; TYPE: PRT

; FEATURE:

; OTHER INFORMATION: Chimeric Peptide consisting of amino acid sequence 1-10 of the

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: RH hormone linked by a spacer to amino acid sequence 288-302 of

; OTHER INFORMATION: the Measles virus protein F linked by a spacer to amino acid se-

; NAME/KEY: MOD-RES

; LOCATION: (1)-(1)

; OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline

; NAME/KEY: MOD-RES

; LOCATION: (47)-(47)

; OTHER INFORMATION: Amidated-Glycine or Glycinamide

; NAME/KEY: PEPTIDE

; LOCATION: (1)-(10)

; OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone

; NAME/KEY: PEPTIDE

; LOCATION: (11)-(18)

; OTHER INFORMATION: Spacer peptide

; NAME/KEY: PEPTIDE

; LOCATION: (19)-(34)

; OTHER INFORMATION: Amino acid sequence 288-302 of the Measles virus fusion protein

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	246	99.2	47	9 US-09-848-834A-17	Sequence 17, Appl
2	173	69.8	34	9 US-09-848-834A-13	Sequence 13, Appl
3	159	64.1	31	9 US-09-848-834A-9	Sequence 9, Appl
4	147.5	59.5	46	9 US-09-848-834A-19	Sequence 19, Appl
5	144	58.1	51	9 US-09-848-834A-20	Sequence 20, Appl
6	141.5	57.1	50	9 US-09-848-834A-18	Sequence 18, Appl
7	116	46.8	45	14 US-10-076-674-9	Sequence 9, Appl
8	116	46.8	45	15 US-10-355-161A-9	Sequence 9, Appl
9	106	42.7	40	14 US-10-237-711-10	Sequence 10, Appl
10	102	41.1	75	10 US-09-847-102A-31	Sequence 31, Appl
11	102	41.1	75	14 US-10-285-976-229	Sequence 229, Appl
12	101	40.7	75	14 US-09-847-102A-33	Sequence 33, Appl
13	101	40.7	75	14 US-10-285-976-231	Sequence 231, Appl
14	96.5	38.9	49	9 US-09-019-010-04	Sequence 4, Appl
15	96.5	38.9	49	10 US-09-305-924-11	Sequence 11, Appl

NAME/KEY: PEPTIDE
 LOCATION: (35) . . . (38)
 OTHER INFORMATION: Spacer peptide

NAME/KEY: PEPTIDE
 LOCATION: (39) . . . (47)
 OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone

US-09-848-834A-17

Query Match 99.2%; Score 246; DB 9; Length 47;
 Best Local Similarity 100.0%; Pred. No. 4.3e-24;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HWSYGLRPGSSGSPSLKLSEIKGVIVHLLEGVEGEGPSLHWSYGLRP 46
 Db 2 HWSYGLRPGSSGSPSLKLSEIKGVIVHLLEGVEGEGPSLHWSYGLRP 46

RESULT 2
 US-09-848-834A-13
 Sequence 13, Application US/09848834A
 Patent No. US20020076416A1

GENERAL INFORMATION:
 APPLICANT: Aphton Corporation
 TITLE OF INVENTION: Chimeric Peptide Immunogens
 FILE REFERENCE: 1102865-0047
 CURRENT APPLICATION NUMBER: US/09/848, 834A
 CURRENT FILING DATE: 2001-05-04
 PRIOR APPLICATION NUMBER: 60/202, 328
 PRIOR FILING DATE: 2000-05-05
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 13
 LENGTH: 34

TYPE: PRT
 ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of the GnRH hormone linked by a spacer to amino acid sequence 288-302 of the Measles virus fusion protein.
 NAME/KEY: PEPTIDE
 LOCATION: (1) . . . (10)

OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone

NAME/KEY: PEPTIDE
 LOCATION: (11) . . . (18)

OTHER INFORMATION: Spacer peptide

NAME/KEY: PEPTIDE
 LOCATION: (19) . . . (34)

OTHER INFORMATION: Amino acid sequence 288-302 of the Measles virus fusion protein, F

NAME/KEY: MOD_RES
 LOCATION: (1) . . . (1)

OTHER INFORMATION: Pyroglutamic acid or 5-oxopropine

US-09-848-834A-13

Query Match 69.8%; Score 173; DB 9; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.7e-15;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HWSYGLRPGSSGSPSLKLSEIKGVIVHLLEGVE 34
 Db 2 HWSYGLRPGSSGSPSLKLSEIKGVIVHLLEGVE 34

RESULT 3
 US-09-848-834A-9
 Sequence 9, Application US/09848834A
 Patent No. US20020076416A1

GENERAL INFORMATION:
 APPLICANT: Aphton Corporation
 TITLE OF INVENTION: Chimeric Peptide Immunogens
 FILE REFERENCE: 1102865-0047
 CURRENT APPLICATION NUMBER: US/09/848, 834A
 CURRENT FILING DATE: 2001-05-04
 PRIOR APPLICATION NUMBER: 60/202, 328
 PRIOR FILING DATE: 2000-05-05
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn version 3.0

SEQ ID NO: 19
 LENGTH: 46

TYPE: PRT
 ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of human GnRH linked by a spacer to amino acid sequence 830-844 of Tantoxylisin linked by a spacer to amino acid

NAME/KEY: MOD_RES
 LOCATION: (1) . . . (1)

OTHER INFORMATION: Pyroglutamic acid or 5-oxoprolidine

NAME/KEY: MOD_RES
 LOCATION: (46) . . . (46)

OTHER INFORMATION: Amidated glycine or glycaminide

NAME/KEY: FBPTIDE
 LOCATION: (1) . . . (10)

OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone

NAME/KEY: PEPTIDES

LOCATION: (11) ..(16)
 OTHER INFORMATION: Spacer peptide
 NAME/KEY: PEPTIDE
 LOCATION: (17) ..(31)
 OTHER INFORMATION: Amino acid sequence 830-834 of the tetanus toxoid precursor
 NAME/KEY: PEPTIDE
 LOCATION: (32) ..(37)
 OTHER INFORMATION: Spacer peptide
 NAME/KEY: PEPTIDE
 LOCATION: (38) ..(46)
 OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
 US-09-848-834A-19

Query Match Score 147.5; DB 9; Length 46;
 Best Local Similarity 62.5%; Pred. No. 1.4e-11;
 Matches 30; Conservatives 4; Mismatches 7; Indels 7; Gaps 2;

Qy 2 HWSYGLRPSSGPSPSLKLI--SEIKGVIVHRLEGEGVGGPSLHWSYGLRP 46
 Db 2 HWSYGLRPSSGPSPSLOVTKANSKFI---TELSSGPSPSLHWSYGLRP 45

RESULT 6
 US-09-848-834A-18
 / Sequence 18, Application US/09848834A
 / Patent No. US20020076416A1
 / GENERAL INFORMATION:
 / APPLICANT: Abtton Corporation
 / TITLE OF INVENTION: Chimeric Peptide Immunogens
 / FILE REFERENCE: 1102865-0047
 / CURRENT APPLICATION NUMBER: US/09/848, 834A
 / CURRENT FILING DATE: 2001-05-04
 / PRIOR APPLICATION NUMBER: 60/202, 328
 / PRIOR FILING DATE: 2000-05-05
 / NUMBER OF SEQ ID NOS: 20
 / SOFTWARE: PatentIn version 3.0
 / SEQ ID NO: 18
 / LENGTH: 50
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of human GnRH linked by a spacer to amino acid sequence 947-957 of the Tanus toxoid precursor (Tetoxylysin). Protein linked by a spacer.
 / OTHER INFORMATION: GnRH linked by a spacer to amino acid sequence 947-957 of the Tanus toxoid precursor (Tetoxylysin). Protein linked by a spacer.
 / OTHER INFORMATION: o amino acid sequence 2-10 of human GnRH
 / NAME/KEY: MOD RES
 / LOCATION: (1) ..(1)
 / OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline
 / NAME/KEY: MOD RES
 / LOCATION: (50) ..(50)
 / OTHER INFORMATION: Amidated glycine or glycaminide
 / NAME/KEY: PEPTIDE
 / LOCATION: (1) ..(10)
 / OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
 / NAME/KEY: PEPTIDE
 / LOCATION: (11) ..(16)
 / OTHER INFORMATION: Spacer peptide
 / NAME/KEY: PEPTIDE
 / LOCATION: (17) ..(37)
 / OTHER INFORMATION: Amino acid sequence 947-957 of the tetanus toxoid precursor (Tanus toxoid precursor (Tetoxylysin)).
 / OTHER INFORMATION: oxylysin
 / NAME/KEY: PEPTIDE
 / LOCATION: (38) ..(41)
 / OTHER INFORMATION: Spacer peptide
 / NAME/KEY: PEPTIDE
 / LOCATION: (42) ..(50)
 / OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
 US-09-848-834A-18

Query Match Score 141.5; DB 9; Length 50;
 Best Local Similarity 59.8%; Pred. No. 9.1e-11;
 Matches 30; Conservatives 1; Mismatches 11; Indels 9; Gaps 2;

Qy 2 HWSYGLRPSSGPSPSLKLI--KILSETKGIVVHRLLEGEGVGGPSLHWSYGLRP 46
 Db 2 HWSYGLRPSSGPSPSFLNNFTVFWLRVPKVSASHL---EGPSLHWSYGLRP 49

RESULT 7
 US-10-076-674-9
 / Sequence 9, Application US/10076674
 / Publication No. US20030165478A1
 / GENERAL INFORMATION:
 / APPLICANT: Sokol, Kenneth K.
 / TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
 / FILE REFERENCE: Immunogen Delivery System
 / CURRENT APPLICATION NUMBER: US/10/076, 674
 / CURRENT FILING DATE: 2002-04-23
 / NUMBER OF SEQ ID NOS: 11
 / SOFTWARE: PatentIn version 3.1

Query Match Score 144; DB 9; Length 51;
 Best Local Similarity 57.1%; Pred. No. 4.5e-11;
 Matches 28; Conservatives 8; Mismatches 9; Indels 4; Gaps 2;

US-09-848-834A-20

SEQ ID NO: 9
LENGTH: 45
TYPE: PRT
ORGANISM: Human
us-10-076-874-9

Query Match Score 116; DB 14; Length 45;
Best Local Similarity 85.7%; Pred. No. 1.4e-07;
Matches 24; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

RESULT 8
US-10-55-161A-9
Sequence 9, Application US/10355161A
Publication No. US201040009897A1
GENERAL INFORMATION:
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/355,161A
CURRENT FILING DATE: 2003-04-31
PRIOR APPLICATION NUMBER: US 10/076674
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO: 9
LENGTH: 45
TYPE: PRT
ORGANISM: Human
us-10-355-161A-9

Query Match Score 116; DB 15; Length 45;
Best Local Similarity 85.7%; Pred. No. 1.4e-07;
Matches 24; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy 19 LSEIKGVIVHLRLEGEGPSLHWSYGLRP 46
Db 19 LSEIKGVIVHLRLEGEGPSLHWSYGLRP 44

RESULT 9
US-10-223-711-10
Sequence 10, Application US/10223711
Publication No. US20050113344A1
GENERAL INFORMATION:
APPLICANT: Bakaletz, Lauren O.
APPLICANT: Kaufman, Pravin T.P.
TITLE OF INVENTION: Synthetic Chimeric Filimbrin Peptides
FILE REFERENCE: 18525/04058
CURRENT APPLICATION NUMBER: US/10/223,711
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 09/148,711
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 08/460,502
PRIOR FILING DATE: 1995-06-02
SOFTWARE: Patentin version 3.1
SEQ ID NO: 10
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial
OTHER INFORMATION: synthetic construct
us-10-223-711-10

Query Match Score 106; DB 14; Length 40;
Best Local Similarity 79.3%; Pred. No. 2.3e-06;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 GLRGSSGSSGPSSLKLSEIKGVIVHLRLEGVE 34
Db 23 GLQSGAGGTGGPGGGAPPRYATLEHPFRCGPSLKLRSVIVHLRLEGVE 75

RESULT 10
US-09-847-102A-31
Sequence 31, Application US/09847102A
Publication No. US20030044409A1
GENERAL INFORMATION:
APPLICANT: University of California
APPLICANT: Carson, Dennis A.
APPLICANT: Corr, Maripat
APPLICANT: Rhee, Chae-Seo
APPLICANT: Lorenzo, Leoni M.
APPLICANT: Malini, Sen
TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
FILE REFERENCE: 22000-2029_00
CURRENT APPLICATION NUMBER: US/09/847,102A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FAST-SEQ for Windows Version 4.0
SEQ ID NO: 31
LENGTH: 75
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: FFZD2-MMVF
us-09-847-102A-31

Query Match Score 102; DB 10; Length 75;
Best Local Similarity 47.2%; Pred. No. 1.5e-05;
Matches 25; Conservative 2; Mismatches 2; Indels 24; Gaps 1;

Qy 6 GLRGSSGSSGPSSLKLSEIKGVIVHLRLEGVE 34
Db 23 GLQSGAGGTGGPGGGAPPRYATLEHPFRCGPSLKLRSVIVHLRLEGVE 75

RESULT 11
US-10-285-976-229
Sequence 229, Application US/10285976
Publication No. US20030165500A1
GENERAL INFORMATION:
APPLICANT: Rhee, Chae-Seo
APPLICANT: Malini, Sen
APPLICANT: Wu, Christina
APPLICANT: Corr, Maripat
APPLICANT: Carson, Dennis A.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
FILE REFERENCE: 023070-130320US
CURRENT APPLICATION NUMBER: US/10/285,976
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: US 60/287,995
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: WO 2002-05-01
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 232
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 229
LENGTH: 75
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: FFZD2-MMVF
OTHER INFORMATION: measles virus fusion (MVF) epitope fused to
OTHER INFORMATION: frizzled domain
us-10-285-976-229

Query Match Score 102; DB 14; Length 75;
 Best Local Similarity 47.2%; Pred. No. 1.5e-05;
 Matches 25; Conservative 2; Mismatches 2; Indels 24; Gaps 1;

Qy 6 GIRPGSS-
 Db 23 GLQPGRGTPGGPGGGGAPPRYATLEHPPHCGPSLKLISLIKGVIVHRLLEGVE 75

RESULT 12
 US-09-847-102A-33 Application US/09847102A
 GENERAL INFORMATION:
 ; APPLICANT: University of California
 ; APPLICANT: Carson, Dennis A.
 ; APPLICANT: Corr, Maripat
 ; APPLICANT: Rhee, Chae Seo
 ; APPLICANT: Lorenco, Leoni M.
 ; APPLICANT: Malini, Sen
 ; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
 ; TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
 ; FILE REFERENCE: 20000-20629_00
 ; CURRENT APPLICATION NUMBER: US/09/847,102A
 ; CURRENT FILING DATE: 2001-05-01
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 33
 ; LENGTH: 75
 ; TYPE: PPT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PMMVF-FD2

Query Match Score 101; DB 10; Length 75;
 Best Local Similarity 91.3%; Pred. No. 2.1e-05;
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 16 LKILSEIKGVIVHRLLEGVEGPSL 38
 Db 1 MKLISLIKGVIVHRLLEGVEGPSL 23

RESULT 14
 US-09-019-010-4 Application US/09019010
 ; Sequence 4, Application US/09019010
 ; Patent No. US20010014330A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HARLAND, RICHARD
 ; APPLICANT: MANN, JOHN G.
 ; APPLICANT: ACRES, STEPHEN D.
 ; TITLE OF INVENTION: IMMUNIZATION AGAINST ENDOGENOUS
 ; NUMBER OF SEQUENCES: 6
 ; NUMBER OF MOLECULES:
 ; TITLE OF INVENTION: MOLECULES
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ROBINS & ASSOCIATES
 ; STREET: 900 MIDDLEFIELD ROAD, SUITE 200
 ; CITY: MENLO PARK
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/019,010
 ; FILING DATE: 05-FEB-1998
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/036,883
 ; FILING DATE: 05-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MCCracken, Thomas P.
 ; REGISTRATION NUMBER: 30,548
 ; REFERENCE DOCKET NUMBER: 9001-0035
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 325-7812
 ; TELEFAX: (650) 325-7823
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 49 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Protein

US-09-019-010-4

Query Match Score 96.5%; DB 9; Length 49;
 Best Local Similarity 44.7%; Pred. No. 4.7e-15;
 Matches 21; Conservative 1; Mismatches 10; Indels 15; Gaps 2;

Qy 2 HWSYGLRPGSSGSPSLKLSLIKGVIVHRLLEGVE--GPSLMSYGRP 46
 Db 2 HWSYGLRPGSSGSDWSY-----GIRPGSSGSSWWSYGRP 35

RESULT 15
 US-09-305-924-11 Application US/09305924A
 ; Sequence 11, Application US/09305924A
 ; Publication No. US20030091579A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jack G. Manns

OTHER INFORMATION: Description of Artificial Sequence: PMMVF-FD2

APPLICANT: Stephen D. Acres
; APPLICANT: Richard Harland
TITLE OF INVENTION: METHODS OF RAISING ANIMALS FOR MEAT PRODUCTION
FILE REFERENCE: 9001-0048
CURRENT APPLICATION NUMBER: US 09/305,924A
CURRENT FILING DATE: 1999-05-05
; ; ;
EARLIER APPLICATION NUMBER: US 60/084,217
; ; ;
EARLIER FILING DATE: 1998-05-05
; ; ;
NUMBER OF SEQ ID NOS: 14
; ; ;
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 11
; ;
LENGTH: 49
; ;
TYPE: PRT
ORGANISM: GnRH
US-09-305-924-A1

Query	2 HWSYGLRPGSSGSSKLSEIKGVVHLLEGVE-GPSLHWSYGRP	46
Match	38.9%	Score 96.5; DB 10; Length 49;
Best Local Similarity	44.7%	Pred. No. 4.7e-05;
Matches	21;	Mismatches 1; Indels 15; Gaps 2;
Conservative		

Search completed: March 10, 2004, 10:25:49
Job time : 36.9416 secs

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GenCore version 5.1.6

SM protein = protein search: using SW model

Run on: March 10, 2004, 08:58:54 ; Search time 13.9377 Seconds
(without alignments)

Title: US-09-848-834A-16

Sequence: 1 XHWSYGLRPSSGPGSLDEKRIAKMERASS

Session 100 - Guest 05
Bulldozer

Searched: 389414 secs. 51625971 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Post-processing: Minimum Match 0%

Lasting first 45 seconds

Database : Issued_Patents_AA;*

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3: /cg2-6_ptodata/2/iaa/6A_COMBO.pep:*
4: /cn2-6_ptodata/2/iaa/6B_COMBO.pep:*
5: /cn2-6_ptodata/2/iaa/PCTUS_COMBO.pep:*
6: /cg2-6_ptodata/2/iaa/backfiles1.pep:*

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	49.7	412	1	US-08-213-288B-18
2	91	49.7	423	2	US-08-760-79FA-1
3	91	49.7	424	2	US-08-760-79FA-3
4	91	49.7	424	3	US-08-932-929B-1
5	91	49.7	424	3	US-08-932-929B-3
6	89	48.6	21	1	US-08-186-266B-6
7	89	48.6	21	1	US-08-146-632-48
8	89	48.6	21	3	US-08-488-351A-48
9	89	48.6	21	3	US-09-100-40A-54
10	89	48.6	21	4	US-08-464-49C-17
11	89	48.6	21	4	US-08-738-822A-12
12	89	48.6	21	4	US-08-197-184C-97
13	89	48.6	21	4	US-09-543-60A-39
14	89	48.6	21	5	PCT-US95-02121-97
15	89	48.6	21	5	PCT-US95-1138A1-20
16	89	48.6	33	1	US-08-466-692-27
17	89	48.6	33	2	US-08-488-495A-27
18	79	43.2	17	4	US-08-464-496-16
19	79	43.2	17	4	US-08-197-494-96
20	79	43.2	17	5	PCT-US95-02121-96
21	75	41.0	16	2	US-08-817-93A-7
22	73	40.2	20	1	US-08-467-167A-20
23	73.5	40.2	20	4	US-08-627-820-20
24	73.5	40.2	20	5	PCT-US92-07228-17
25	71	38.8	17	1	US-08-188-223-6
26	71	38.8	17	3	US-08-966-466-6
27	70	38.0	16	1	US-08-188-223-6

ALIGNMENTS

RESULT 2
US-08-760-797A-1
Sequence 1, Application US/08760797A
Patent No. 5928902

GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmidium and HBsAG
NUMBER OF SEQUENCES: 4

ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: B45015-1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5096
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-760-797A-3

Query Match Score 91; DB 2; Length 423;
Best Local Similarity 55.3%;
Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/760,797A
FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PRIORITY APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: B45015-1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5096
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-760-797A-1

Query Match Score 91; DB 2; Length 424;
Best Local Similarity 55.3%;
Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,797A
FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PRIORITY APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: B45015-1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096

RESULT 3
US-08-760-797A-3
Sequence 3, Application US/08760797A
Patent No. 5928902

GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmidium and HBsAG
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
STATE: PA
COUNTRY: USA
ZIP: 19406

CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406

COMPILER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0

RESULT 4
US-08-932-929B-1
Sequence 1, Application US/08932929B
Patent No. 6169171

GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmidium and HBsAG
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406

COMPILER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0

RESULT 5
US-08-932-929B-2
Sequence 2, Application US/08932929B
Patent No. 6169171

GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmidium and HBsAG
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
STATE: PA
COUNTRY: USA
ZIP: 19406

COMPILER READABLE FORM:

TELEFAX: 610-270-5090
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 424 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 US-08-932-929B-1

Query Match 49.7%; Score 91; DB 3; Length 424;
 Best Local Similarity 55.3%; Pred. No. 6.3e-05; Indels 8; Gaps 1;
 Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

Db 7 LRPGSSCPSLD-----EKKIAKMEKASSVENVNS 36
 Db 156 IKPGSANKPKDDELVDIERRKICMKCSVENVNS 193

RESULT 5
 US-08-932-929B-3
 / Sequence 3, Application US/08932929B
 / Patent No. 6169171
 / GENERAL INFORMATION:
 / APPLICANT: De Wilde, Michel
 / TITLE OF INVENTION: Hybrid Protein Between CS
 / TITLE OF INVENTION: From Plasmodium and HBAG
 / NUMBER OF SEQUENCES: 4
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: SmithKline Beecham Corporation
 / STREET: 709 Swedeland Road
 / CITY: King of Prussia
 / STATE: PA
 / COUNTRY: USA
 / ZIP: 19406

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/932,929B
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/027,746
 FILING DATE: 05-MAR-1993
 PRIORITY DATA:
 APPLICATION NUMBER: US 07/926,666
 FILING DATE: 29-NOV-1993
 PRIORITY DATA:
 APPLICATION NUMBER: US 08/103,396
 FILING DATE: 06-AUG-1993
 PRIORITY/AGENT INFORMATION:
 NAME: Bartiar, Kevin L.
 APPLICATION NUMBER: 34,774
 REGISTRATION NUMBER: 14137-50-4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-3600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: 1..21
 OTHER INFORMATION: /note= "Plasmodium falciparum CS
 US-08-186-266-6

Query Match 48.6%; Score 89; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4e-06; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0;

Db 18 EKKIAKMEKASSVENVNS 36
 Db 3 EKKIAKMEKASSVENVNS 21

RESULT 7

Query Match 49.7%; Score 91; DB 3; Length 424;
 Best Local Similarity 55.3%; Pred. No. 6.3e-05; Indels 8; Gaps 1;
 Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

Db 7 LRPGSSCPSLD-----EKKIAKMEKASSVENVNS 36
 Db 152 IKPGSANKPKDDELVDIERRKICMKCSVENVNS 189

US-08-446-692-48
 Sequence 48, Application US/08446692
 Patent No. 5759551
 GENERAL INFORMATION:
 APPLICANT: Ladd, Anna
 APPLICANT: Wang, Chang Yi
 APPLICANT: Zamb, Timothy
 TITLE OF INVENTION: Immunogenic LHRH peptide constructs
 TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
 NUMBER OF SEQUENCES: 114
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Maria C.H. Lin
 STREET: 345 Park Avenue
 CITY: New York
 STATE: NY
 COUNTRY: US
 ZIP: 10154-0053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/446, 692
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Maria C.H. Lin
 REGISTRATION NUMBER: 29, 323
 REFERENCE/DOCKET NUMBER: 1151-4146 US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 415-8745
 TELEFAX: (516) 751-8849
 INFORMATION FOR SEQ ID NO: 48:
 LENGTH: 21 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-446-692-48

RESULT 8
 Query Match 48.6%; Score 89; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EKKIAKMEKASSVNVVNS 36
 Db 3 EKKIAKMEKASSVNVVNS 21

RESULT 8
 US-08-488-351A-48
 Sequence 48, Application US/08488351A
 Patent No. 5843446
 GENERAL INFORMATION:
 APPLICANT: Ladd, Anna
 APPLICANT: Wang, Chang Yi
 APPLICANT: Zamb, Timothy
 TITLE OF INVENTION: Immunogenic LHRH peptide constructs
 TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
 NUMBER OF SEQUENCES: 114
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Maria C.H. Lin
 STREET: 345 Park Avenue
 CITY: New York
 STATE: NY
 COUNTRY: US
 ZIP: 10154-0053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/100, 409A

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/488, 351A
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/446, 692
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/229, 275
 FILING DATE: 14-APR-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/057, 166
 FILING DATE: 27-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Maria C.H. Lin
 REGISTRATION NUMBER: 29, 323
 REFERENCE/DOCKET NUMBER: 1151-4146 US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 415-8745
 TELEFAX: (516) 751-8849
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-488-351A-48

RESULT 9
 US-08-100-409A-54
 Sequence 54, Application US/09100409A
 Patent No. 6090188
 GENERAL INFORMATION:
 APPLICANT: Wang, Chang Yi
 TITLE OF INVENTION: PEPTIDE COMPOSITION FOR PREVENTION AND TREATMENT OF HIV INFECTION AND IMMUNE DISORDERS
 TIME OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND IMMUNE DISORDERS
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: 4 MORGAN & FINNEMAN
 STREET: 345 Park Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10154-0054
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/100, 409A
 FILING DATE: 14-APR-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME:
 REFERENCE/DOCKET NUMBER: 1151-4154
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-758-8800

TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLGY: linear
; MOLECULE TYPE: Peptide
US-09-100-409A-54

Query Match 48.6%; Score 89; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Pred. No. 4e-06; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EKKIAKMEKASSVFNVNS 36
Db 3 EKKIAKMEKASSVFNVNS 21

RESULT 10
; Sequence 17, Application US/08464496
; Patent No. 6322789
; GENERAL INFORMATION:
; APPLICANT: Epimmune, Inc.
; APPLICANT: Vitiello, Maria
; APPLICANT: Chesnut, Robert
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
; FILE REFERENCE: EPITOPPS
; CURRENT APPLICATION NUMBER: 39963-20001.13
; CURRENT FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 07/935,811
; PRIOR FILING DATE: 1992-08-16
; PRIOR APPLICATION NUMBER: 07/874,491
; PRIOR FILING DATE: 1992-04-27
; PRIOR APPLICATION NUMBER: 07/827,682
; PRIOR FILING DATE: 1992-01-29
; PRIOR APPLICATION NUMBER: 07/749,568
; PRIOR FILING DATE: 1991-08-26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Malaria circumsporozoite 378-398

Query Match 48.6%; Score 89; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Pred. No. 4e-06; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EKKIAKMEKASSVFNVNS 36
Db 3 EKKIAKMEKASSVFNVNS 21

RESULT 11
US-08-788-822A-12
; Sequence 12, Application US/08788822A
; Patent No. 6419325
; GENERAL INFORMATION:
; APPLICANT: Alexander, Jeffrey L.
; APPLICANT: Deffrees, Shawn
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Induction of Immune Response Against
; TITLE OF INVENTION: Desired Determinants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA

ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,822A
; FILING DATE: 23-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,510
; FILING DATE: 24-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE DOCKET NUMBER: 014137-009210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-788-822A-12

Query Match 48.6%; Score 89; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e-06; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EKKIAKMEKASSVFNVNS 36
Db 3 EKKIAKMEKASSVFNVNS 21

RESULT 12
US-08-197-484-97
; Sequence 97, Application US/08197484
; Patent No. 6419331
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US

ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,682
 FILING DATE: 29-JAN-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/749,568
 FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:
 NAME: Parmelee, Steven W.
 REGISTRATION NUMBER: 31,990
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 467-3600
 TELEFAX: (206) 623-6793

INFORMATION FOR SEQ ID NO: 97:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: Peptide

NAME/KEY: Peptide
 LOCATION: 1..21
 OTHER INFORMATION: /note= "Malaria circumsporozoite
 OTHER INFORMATION: 378-398"
 US-08-197-484-97

Query Match 48.6% Score 89; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4e-06; Indels 0; Gaps 0;

Qy 18 EKKIAKMEKASSVNVNS 36
 Db 3 EKKIAKMEKASSVNVNS 21

RESULT 13
 US-09-543-608A-39
 ; Sequence 39, Application US/09543608A
 ; Patent No. 660210
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John D.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Celis, Esteban
 ; APPLICANT: Keogh, Elissa A.
 ; APPLICANT: Cheanut, Robert
 ; APPLICANT: Epimmune Inc.
 ; TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
 ; TITLE OF INVENTION: Peptides and Vaccine Compositions
 ; FILE REFERENCE: 018623-015710US
 ; CURRENT APPLICATION NUMBER: US 09/543,608A
 ; CURRENT FILING DATE: 2002-04-05
 ; SOFTWARE: FastSEQ For Windows Version 3.0
 ; SEQ ID NO: 39
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Plasmodium falciparum CS protein positions 378-398
 US-09-543-608A-39

Query Match 48.6% Score 89; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4e-06; Indels 0; Gaps 0;

Qy 18 EKKIAKMEKASSVNVNS 36
 Db 3 EKKIAKMEKASSVNVNS 21

RESULT 14
 PCT-US5-02121-97
 ; Sequence 97, Application PC/TUS9502121
 ; GENERAL INFORMATION:
 ; APPLICANT: COMPOSITIONS AND METHODS FOR ELICITING
 ; TITLE OF INVENTION: CTL IMMUNITY
 ; NUMBER OF SEQUENCES: 153
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/02121
 ; FILING DATE: 16-FEB-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/197,484
 ; FILING DATE: 16-FEB-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/935,811
 ; FILING DATE: 26-AUG-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/874,491
 ; FILING DATE: 27-APR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/827,682
 ; FILING DATE: 29-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/749,568
 ; FILING DATE: 26-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 14137-26-4-PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 467-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 97:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 21 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: Peptide
 ; FEATURE:
 ; NAME/KEY: Peptide
 ; LOCATION: 1..21
 ; OTHER INFORMATION: /note= "Malaria circumsporozoite
 ; OTHER INFORMATION: 378-398"
 PCT-US5-02121-97

Query Match 48.6% Score 89; DB 5; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4e-06; Indels 0; Gaps 0;

Qy 18 EKKIAKMEKASSVNVNS 36
 Db 3 EKKIAKMEKASSVNVNS 21

RESULT 15
 PCT-US5-13841-20
 ; Sequence 20, Application PC/TUS9513841
 ; GENERAL INFORMATION:
 ; APPLICANT: United Biomedical Inc; Walfield, Alan M.;
 ; APPLICANT: Wang, Chang Y.;
 ; TITLE OF INVENTION: Synthetic IgE Membrane Anchor
 ; TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Maria C.H. Lin

STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13841
FILING DATE: 25-OCT-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/328,519
FILING DATE: 25-OCT-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lin, Maria C.H.
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4117
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-13841-20

Query Match 48.6%; Score 89; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. NO. 4e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 EKKIAKMEKASSVENTNS 36
Db 3 EKKIAKMEKASSVENTNS 21

Search completed: March 10, 2004, 09:28:56
Job time : 14.9377 secs

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Searched: 283366 seqs, 96191526 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

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1: pirl:*

Database : PIR_78:
1: _pir1:
1:

5: First: *
6: 3: Dir3: *
7: 4: Dir4: *

5: First: *
6: 3: Dir3: *
7: 4: Dir4: *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. This is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	97	53.0	388	2	Circumsporozoite p
2	91	49.7	405	2	Circumsporozoite p
3	91	49.7	412	1	Circumsporozoite p
4	91	49.7	424	1	Circumsporozoite p
5	90	49.2	442	2	Circumsporozoite p
6	58	31.7	10	1	Gonadoliberin - PI
7	58	31.7	10	1	Gonadoliberin - SH
8	58	31.7	67	2	Gonadoliberin prec
9	58	31.7	89	2	Gonadoliberin prec
10	58	31.7	90	1	Gonadoliberin prec
11	58	31.7	92	1	Gonadoliberin prec
12	58	31.7	92	1	Gonadoliberin prec
13	58	31.7	332	1	Circumsporozoite p
14	58	31.7	348	1	Circumsporozoite p
15	55	30.1	98	2	Gonadotropin-releas
16	55	30.1	264	2	Circumsporozoite p
17	55	30.1	367	1	Circumsporozoite p
18	54	29.5	10	1	Gonadoliberin I -
19	54	29.5	92	2	Gonadoliberin I pr
20	53	29.2	90	2	Gonadalotropin-prot
21	53	29.0	70	2	hypothetical prote
22	53	29.0	70	2	methylamino-ase
23	52.5	28.7	501	2	hypothetical prote
24	52	28.4	487	2	hypothetical prote
25	52	28.4	719	2	hypothetical prote
26	51.5	28.1	1401	2	hypothetical prote
27	51.5	28.1	80	1	gonadoliberin I pr
28	51.5	28.1	90	2	salmon-type gonado
29	51	28.1	444	2	trigger factor MG22
29	51	27.9	315	2	hypothetical prote
29	51	27.9	444	2	trigger factor MG22
29	51	27.9	444	2	hypothetical prote

RESULT 1
A39756
circumsp
C.Species:
C.Date:
C.Access:
R.Lal, A
J. Biol.
A.Title:
A.Referer:
A.Access:
A.Status:
A.Molecu
A.Residu
A.Cross-
C.Superf
F:312-36

ALIGNMENT S

Mol. Biochem. Parasitol. 37, 275-280, 1989
 A;Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell epitopes
 A;Reference number: A60657; MUID:90114334; PMID:2481827
 A;Accession: 160557
 A;Molecule type: DNA
 A;Cross-references: GB:K02194; PIDN:9160160; PID:9160161
 A;Experimental source: clone 7G8
 C;Comment: Residues 1-16 are the probable signal sequence.
 C;Comment: There are 41 copies of a 4-residue unit in the middle domain of the protein.
 C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology <THR1>
 F;348-383/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match Score 91; DB 2; Length 405;
 Best Local Similarity 55.3%; Pred. No. 0.00012; Indels 8; Gaps 1;
 Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

Qy 7 LRPSSGSPLD-----EKKIAKMEASSVENVNS 36
 Db 361 IKPGSANKPKDLDYNDIEKKICRKMECKSSVENVNS 391

RESULT 3
 OZQQAf
 Circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate IMTM22)
 C;Species: Plasmodium falciparum
 C;Date: 15-Nov-1994 #sequence_revision 15-Nov-1994 #text_change 09-Jun-2000
 C;Accession: A03388
 R;Name: J.B.; Williams, J.L.; McCutchan, T.F.; Weber, J.L.; Wirtz, R.A.; Hochmeyer, W.T.
 Science 225, 593-599, 1984
 A;Title: Structure of the gene encoding the immunodominant surface antigen or the sporozoite of Plasmodium falciparum. MUII:84200215; PMID:6204383
 A;Accession: A03388
 A;Molecule type: DNA
 A;Residues: 1-412 <DBB>
 A;Cross references: GB:K02194; PIDN:9160160; PID:9160161
 A;Experimental source: clone 7G8
 C;Comment: Residues 1-16 are the probable signal sequence.
 C;Comment: There are 41 copies of a 4-residue unit in the middle domain of the protein.
 C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology <THR1>
 F;348-390/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match Score 91; DB 1; Length 412;
 Best Local Similarity 55.3%; Pred. No. 0.00013; Indels 8; Gaps 1;
 Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

Qy 7 LRPSSGSPLD-----EKKIAKMEASSVENVNS 36
 Db 361 IKPGSANKPKDLDYNDIEKKICRKMECKSSVENVNS 398

RESULT 4
 A54533
 Circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain T4, Thailand)
 C;Species: Plasmodium falciparum
 C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
 C;Accession: A54533
 R;Name: del Portillo, H.A.; Nussenzweig, R.S.; Enea, V.
 Mol. Biochem. Parasitol. 24, 289-294, 1987
 A;Title: Circumsporozoite gene of a Plasmodium falciparum strain from Thailand.
 A;Reference number: A54533; MUID:87315205; PMID:3303373
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-424 <DBL>
 A;Cross-references: GB: M19752; PIDN:9160216; PID:9160217
 C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology <THR1>
 F;348-402/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match Score 91; DB 2; Length 424;
 Best Local Similarity 55.3%; Pred. No. 0.00013; Indels 8; Gaps 1;
 Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

Qy 7 LRPSSGSPLD-----EKKIAKMEASSVENVNS 36
 Db 373 IKPGSANKPKDLDYNDIEKKICRKMECKSSVENVNS 410

RESULT 5
 A54529
 Circumsporozoite protein, malaria parasite (Plasmodium falciparum) (strain Wellcome)
 C;Species: Plasmodium falciparum
 C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
 C;Accession: A54529
 R;Lockyer, N.J.; Schwarz, R.T.
 Mol. Biochem. Parasitol. 22, 101-105, 1987
 A;Title: Strain variation in the circumsporozoite protein gene of Plasmodium falciparum
 A;Reference number: A54529; MUID:87115616; PMID:3543671
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-442 <LOC>
 A;Cross references: GB: M15505; PIDN:AAA29554; PID:9160215
 C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology <THR1>
 C;Keywords: tandem repeat
 F;366-420/Domain: thrombospondin type 1 repeat homology <THR1>

RESULT 6

RHPGG
 Gonadotropin - pig
 Sus scrofa domestica (domestic pig)
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 18-Mar-1997
 C;Accession: A01411
 R;Baba, Y.; Matsuo, H.; Schally, A.V.
 Biochem. Biophys. Res. Commun. 44, 459-463, 1971
 A;Title: Structure of the porcine LH- and FSH-releasing hormone. II. Confirmation of the structure of the porcine LH- and FSH-releasing hormone. I. Synthesis
 A;Reference number: A90172; MUID:72114303; PMID:4946067
 A;Accession: A01411
 A;Molecule type: Protein
 A;Residues: 1-10 <BAB>
 R;Matsuo, H.; Arimura, A.; Nair, R.M.G.; Schally, A.V.
 Biochem. Biophys. Res. Commun. 45, 822-827, 1971
 A;Title: Synthesis of the porcine LH- and FSH-releasing hormone by the solid-phase method
 A;Contents: annotation; synthesis
 A;Note: the synthetic and natural hormones have the same physicochemical and biological activities
 R;Baba, Y.; Arimura, A.; Schally, A.V.
 Biochem. Biophys. Res. Commun. 45, 483-487, 1971
 A;Title: On the tryptophan residue in porcine LH and FSH-releasing hormone.
 A;Reference number: A90176; MUID:72055376; PMID:4942726
 A;Contents: annotation
 A;Note: TRP-3 appears to be essential for biological activity of both luteinizing and fSH-releasing hormones.
 C;Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and fSH-releasing hormones.
 C;Superfamily: Gonadotropin
 C;Keywords: amidated carboxyl end; amidated carboxyl end; pyroglutamic acid (Gln) #status experimental
 F;1/Modified site: pyrrolidine carboxylic acid (Gly) #status experimental
 F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match Score 58; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.074; Indels 0; Gaps 0;

Qy 2 HWSYGHRPG 10
 Db 2 HWSYGHRPG 10

RESULT 7

RHSG
 gonadotropin - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: A93780; MUID:10411
C;Date: 31-Dec-1991 #text_change 18-Mar-1997
C;Sequence_revision: 31-Dec-1991 #text_change 18-Mar-1997
C;Accession: A93780; MUID:10411
C;Species: R.Burgus, R.; Butcher, M.; Amoss, M.; Ling, N.; Monahan, M.; Rivier, J.; Fellows, R.; Bl
C;Proc. Natl. Acad. Sci. U.S.A. 69, 278-282, 1972
C;Title: Primary structure of the ovine hypothalamic luteinizing hormone-releasing factor
C;Reference number: A93780; MUID:72093314; PMID:4550508
C;Accession: A93780
A;Molecule type: Protein
A;Residues: 1-10 <HVR>
A;Note: the natural and synthetic hormones have the same biological activity
A;Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and follicle-stimulating hormones.
C;Superfamily: Gonadoliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F;1;Modified site: Pyrrolidine carboxylic acid (Gln) #status experimental
F;10;Modified site: amidated carboxyl end (Gly) #status experimental

Query	Match	Score	DB	Length
	Best Local Similarity 100.0%; Matches 9; Conservative 0; Gaps 0;	31.7%	1	10;
Qy	2 HWSYGLRPG 10	0	0	
Db	2 HWSYGLRPG 10	0	0	

RESULT 8

I178541
Gonadoliberin precursor - rhesus macaque (fragment)
N;Alternate names: luteinizing hormone releasing hormone
C;Species: Macaca mulatta (rhesus macaque)
C;Accession: I178541
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C;Sequence_revision: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C;Accession: I178541
C;Species: Macaca mulatta (rhesus macaque)
C;Accession: I178541
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C;Sequence_revision: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
A;Title: Neuroendocrinology 60, 346-359, 1994
A;Title: Developmental expression of the genes encoding transforming growth factor alpha
A;Title: Reference number: 158134; MUID:95124501; PMID:7545971
A;Accession: I178541
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Cross-references: 1-67 <RNS>
C;Superfamily: gonadoliberin

Query	Match	Score	DB	Length
	Best Local Similarity 100.0%; Matches 9; Conservative 0; Gaps 0;	31.7%	2	67;
Qy	2 HWSYGLRPG 10	0	0	
Db	7 HWSYGLRPG 15	0	0	

RESULT 9

I151423
Gonadoliberin precursor - African clawed frog
N;Alternate names: luteinizing hormone releasing hormone
C;Species: Xenopus laevis (African clawed frog)
C;Accession: I151423
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Sequence_revision: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
A;Title: Endocrinology 134, 1835-1845, 1994
A;Title: The frog GnRH-I gene has a mammalian-like expression pattern and conserved domain
A;Reference number: I151423; MUID:94185563; PMID:8137750
A;Accession: I151423
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-89 <HAY>
A;Cross-references: GB:L28040; NID:9496291; PMID:AAA49728; 1; PID:9496292
C;Genetics:
A;Gene: GnRH-I
C;Superfamily: gonadoliberin

R;Seeburg, P.H.; Adelman, J.P.	
Nature 31(1); 666-684, 1984	
A;Title: Characterization of cDNA for precursor of human luteinizing hormone releasing hormone	
A;Reference number: A93342; MUID:85012739; PMID:6090951	
A;Accession: A93342	
A;Molecule type: mRNA	
A;Accession number: A90108; MUID:83126573; PMID:6760865	
A;Cross-references: GB:X01059; NID:gi34356; PIDN:CAA25526_1; PMID:g34357	
A;Experimental source: Placenta	
R;Tan, L.; Rousseau, P.	
Biochem. Biophys. Res. Commun. 109, 1061-1071, 1982	
A;Title: The chemical identity of the immunoreactive LHRH-like peptide biosynthesized in the rat placenta	
A;Reference number: A90108; MUID:83126573; PMID:6760865	
A;Accession: A90108	
A;Molecule type: protein	
A;Residues: 24-33 <TAN>	
A;Experimental source: placental trophoblasts	
R;Leibovitz, D.; Koch, Y.; Pitzer, F.; Frikkin, M.; Dantes, A.; Baumeister, W.; Amsterdam, The Netherlands	
FEBS Lett. 346, 203-206, 1994	
A;Title: Segregated degradation of the neuropeptide gonadotropin-releasing hormone by the placenta	
A;Reference number: S45718; MUID:94283597; PMID:801334	
A;Contents: annotation; degradation pathway of synthetic hormone	
C;Generics:	
A;Gene: GDB:GNRH; LHRH; GRH	
A;Cross-references: GDB:133746; OMIM:227200; OMIM:152760	
A;Map Position: 8P21-8P11.2	
A;Introns: 47/3; 79/3	
C;Function:	
A;Description: Gonadoliberin stimulates pituitary secretion of lutropin and follitropin	
A;Note: Gonadoliberin-associated protein may have prolactin release inhibiting activity	
C;Superfamily: Gonadoliberin	
C;Keywords: amidated carboxyl end; hormone; hypothalamus; placenta; pyroglutamic acid	
F;1-23:Domain: signal sequence #status predicted <SIG>	
F;24-92:Product: Progonadoliberin #status predicted <PGN>	
F;24-33:Product: Gonadoliberin #status experimental <PAT>	
F;37-92:Product: Gonadoliberin-associated protein #status predicted <GAP>	
F;24/Modified site: pyroglutamine carboxylic acid (Gln) (in mature form) #status experimentally confirmed	
F;33/Modified site: amidated carboxylic acid (Gly) (amide in mature form) from following gly	
Query Match 31.7% Score 58; DB 1; Length 92;	
Best Local Similarity 100.0%; Pred. No. 0.86;	
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 2 HWSYGLRPG 10	
Db 25 HWSYGLRPG 33	
RESULT 12	
RHRTG	
Gonadoliberin precursor - rat	
N;Alternate names: Gonadoliberin-associated protein (GAP); gonadotropin releasing hormone	
N;Contains: Gonadoliberin; prolactin release-inhibiting factor	
C;Species: Rattus norvegicus (Norway rat)	
C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 18-Jun-1999	
C;Accession: A40147; B26573; A48410	
R;Bond, C.T.; Haylick, J.S.; Seебurg, P.H.; Adelman, J.P.	
Mol. Endocrinol. 3, 1257-1262, 1989	
A;Title: The rat gonadotropin-releasing hormone: SH locus: structure and hypothalamic expression	
A;Reference number: A40147; MUID:89384661; PMID:2476669	
A;Accession: A40147	
A;Molecule type: DNA	
A;Residues: 1-92 <BON>	
A;Cross-references: GB:M31670; NID:gi204447; PIDN:NAA41264_1; PMID:g204448	
R;Adelman, J.P.; Mason, A.J.; Haylick, J.S.; Seебurg, P.H.	
Proc. Natl. Acad. Sci. U.S.A. 83, 179-183, 1986	
A;Title: Isolation of the gene and hypothalamic cDNA for the common precursor of gonadotropin-releasing hormone and thyrotropin-releasing hormone	
A;Reference number: A94090; MUID:86094338; PMID:2867548	
A;Accession: B26173	
A;Molecule type: mRNA	
A;Residues: 1-92 <ADB>	
A;Cross-references: GB:M12579; NID:gi204445; PIDN:AAA41263_1; PMID:g204446	
R;Meier, C.C.; Marchetti, B.; LeBoeuf, R.D.; Blalock, J.E.	

F;258-310/Domain: thrombospondin type 1 repeat homology <THR1>
 Query Match Score 58; DB 1; Length 332;
 Best Local Similarity 37.1%; Pred. No. 3.5;
 Matches 13; Conservative 9; Mismatches 7;
 Indels 6; Gaps 1;

Qy 8 RPGSSGSPSID-----EKKIARMKERRQSVENVNS 36
 Db 284 RKGSSNKRAEDLTIDITEICKMDKCSSIFNIVSN 318

RESULT 14

Circumsporozoite protein precursor - Plasmodium berghei (strain ANKA clone 2.34L)

N;Alternative names: sporozoite surface antigen

C;Species: Plasmodium berghei

C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999

C;Accession: S07873; S12571

R;Lockyer, M.J.; Davies, C.S.; Subhtier, A.; Sinden, R.E.

R;Nucleic Acids Res 18, 3765, 1990

A;Title: Nucleotide sequence of the Plasmodium berghei circumsporozoite protein gene from

A;Reference number: S07873; PMID:90221834; PMID:2183186

A;Accession: S07873

A;Molecule type: DNA

A;Residues: 1-348 <LOC>

A;Cross-references: EMBL:X17606

R;Lockyer, M.J.

submitted to the EMBL Data Library, November 1989

A;Accession number: S12571

A;Molecule type: DNA

A;Residues: 1-59, I, 61-81, 83-248 <LOC2>

A;Cross-references: EMBL:X17606; PMID:99794; PID:CAA35608.1; PID:g9785

C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

C;Keywords: tandem repeat

F;1-20/Domain: signal sequence #status Predicted <SIG>

F;21-348/Product: circumsporozoite protein #status Predicted <MAT>

F;34-245/Region: 8-residue repeats

F;215-247/Region: 2-residue repeats

F;274-326/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match Score 31.7%; DB 1; Length 348;

Best Local Similarity 37.1%; Pred. No. 3.7;

Matches 13; Conservative 9; Mismatches 7;
 Indels 6; Gaps 1;

Qy 8 RPGSSGSPSID-----EKKIARMKERRQSVENVNS 36
 Db 300 RKGSSNKRAEDLTIDITEICKMDKCSSIFNIVSN 334

RESULT 15

150739 gonadotropin-releasing hormone - Cichlid (Haplochromis burtoni)

C;Species: Haplochromis burtoni

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C;Accession: I50739

R;White, S.A.; Kasten, T.L.; Bond, C.T.; Adelman, J.P.; Fernald, R.D.

Proc. Natl. Acad. Sci. U.S.A. 92, 8363-8367, 1995

A;Title: Three Gonadotropin-releasing hormone genes in one organism suggest novel roles

A;Reference number: I50739; PMID:95396797; PMID:7667296

A;Accession: I50739

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-98 <WHI>

A;Cross-references: EMBL:U31865; PMID:9905398; PID: AAC59691.1; PID:g905399

C;Superfamily: gonadoliberin

Query Match Score 30.1%; DB 2; Length 98;

Best Local Similarity 35.9%; Pred. No. 2.4;

Matches 14; Conservative 4; Mismatches 11; Indels 10; Gaps 2;

Qy 2 HWSYGLRPSASSGPGLD-----KKIARMKASSWF 31

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OM protein - protein search, using SW model

Run on: March 10, 2004, 08:58:53 ; Search time 6.58366 Seconds
(without alignment)
284.724 Million cell updates/sec

Title: US-09-848-834A-16

Perfect score: 183

Sequence: 1 XHWSYGLRGSSGGPSLDEKKAKMEKASSVFTVNS 36

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	53.0	388	1 CSP_PLARE	P26694 Plasmodium
2	91	49.7	397	1 CSP_PLARO	P1597 Plasmodium
3	91	49.7	412	1 CSP_PLAFA	P0283 plasmodium
4	91	49.7	424	1 CSP_PLAFT	P1814 Plasmodium
5	90	49.2	442	1 CSP_PLAFW	P03107 plasmodium
6	61.1	33.6	61	1 GONI_SHEEP	Q25588 ovis aries
7	59	32.2	63	1 GONI_MESAU	Q01163 mesocricetus
8	58	31.7	67	1 GONI_MACMU	P52247 macaca mulatta
9	58	31.7	89	1 GONI_XENLA	P46565 xenopus laevis
10	58	31.7	90	1 GONI_MOUSE	P15622 mus musculus
11	58	31.7	90	1 GONI_RANCA	Q9y63 rana catesbeiana
12	58	31.7	91	1 GONI_BIGSCROFA	P49921 sus scrofa
13	58	31.7	92	1 GONI_HUMAN	P01448 homo sapiens
14	58	31.7	92	1 GONI_RAT	P0490 ratmus norvegicus
15	58	31.7	92	1 GONI_TUPGB	Q93355 tupaias glis
16	58	31.7	339	1 CSP_PLABE	P09915 plasmodium
17	58	31.7	347	1 CSP_PLABA	P23093 plasmodium
18	56.5	30.9	90	1 GONI_DICLIA	Q9a093 diceratarchus
19	55.5	30.3	89	1 GONI_DORNO	P59222 porichthys
20	55	30.1	94	1 GONI_HAPBU	P54318 haplochromis
21	55	30.1	367	1 CSP_PLAYO	P09914 plasmodium
22	55	30.1	721	1 THIC_SHEON	Q8bed7 shewarella
23	54	29.5	10	1 GONI_ALLMI	P37041 alligator mississippiensis
24	54	29.5	92	1 GONI_CHICK	P37042 gallus gallus
25	53.5	29.2	90	1 GONI_HAPBU	P46652 haplochromis
26	52.5	28.7	487	1 MMSA_BACSU	P24212 bacillus subtilis
27	52	28.4	95	1 GONI_NORSA	Q73812 morone saxatilis
28	52	28.4	95	1 GONI_PAGNA	P70074 pagrus major
29	52	28.4	95	1 GONI_SPANU	P51919 sparaxis aurata
30	52	28.4	99	1 GONI_DICLIA	Q9a10 dicentarchus
31	51.5	28.1	80	1 GONI_CLAGA	P33439 claris gariepinus
32	51.5	28.1	90	1 GONI_ORVALA	Q9dd49 o proctonotus
33	51.5	28.1	444	1 TIG_TWICGE	P47480 mycoplasma

ALIGNMENTS

RESULT 1		CSP_PLARE		STANDARD;	
ID	CSP_PLARE	ID	P26694;	PRT:	388 AA.
AC		AC	P26694;		
DT	01-AUG-1992	DT	01-AUG-1992	(Rel. 23, Created)	
				(Rel. 23, Last sequence update)	
				(Rel. 43, Last annotation update)	
DE	Circumsporozoite protein precursor (CS).				
OS	Plasmodium reichenowi.				
OC	Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.				
RN	[1]				
NCBI_TaxID	5854;				
RN					
SEQUENCE FROM N.A.					
RP					
RX					
RA	Lal A.A., Goldblatt I.F.;				
RT	"Circumsporozoite protein gene from Plasmodium reichenowi, a chimpanzee malaria parasite Plasmodium falciparum."				
RT	malaria parasite Plasmodium falciparum.				
RL	J. Biol. Chem. 266:6686-6689(1991).				
CC	- - FUNCTION: The circumsporozoite protein is the immunodominant surface antigen on the sporozoite (the infective stage of the malaria parasite) that is transmitted from the mosquito to the vertebrate host.				
CC	- - MISCELLANEOUS: The C-terminal region is probably used for anchoring the protein to the cell membrane. The repeat sequences would be the surface antigen of the organism.				
CC	- - SIMILARITY: Contains 1 TSP type-1 domain.				
CC					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.ebi.ac.uk/EBI-Software/announce) or send an email to license@ebi.ac.uk.				
CC					
CC	EMLB; M60912; AAA29561.1; -.				
DR	PIR: A39756; A929561.1; -.				
DR	InterPro: IPR03067; Circospzoite.				
DR	InterPro: IPR000884; TSP1.				
DR	PFam: PF00090; tsp_1.				
DR	PRINTS: PS01303; CROMSPZOITE.				
DR	SMART: SM0209; TSP1.				
DR	PROSITE: PS50094; TSP1.				
CC	DR PIR: A39756; A929561.1; -.				
DR	InterPro: IPR03067; Circospzoite.				
DR	InterPro: IPR000884; TSP1.				
DR	PFam: PF00090; tsp_1.				
DR	PRINTS: PS01303; CROMSPZOITE.				
DR	SMART: SM0209; TSP1.				
DR	PROSITE: PS50094; TSP1.				
KW	Malaria; Sporozoite; Repeat; Signal.				
FT	PROBABLE.				
FT	SIGNAL				
FT	16				
FT	CHAIN				
FT	17				
FT	388				
FT	DOMAIN				
FT	120				
FT	263				
P.					

SEQUENCE FROM N.A.
 MEDLINE=89364938; PubMed=2671723;
 RX Caspers P., Ganz T.R., Matile H., Pink J.R., Sinigaglia F.;
 RA "The circumsporozoite protein gene from NF54, a Plasmodium falciparum
 isolate used in malaria vaccine trials."
 RT Mol. Biochem. Parasitol. 35:185-190 (1989)./
 RL -/- FUNCTION: The circumsporozoite protein is the immunodominant
 surface antigen on the sporozoite (the infective stage of the
 malaria parasite that is transmitted from the mosquito to the
 vertebrate host).
 CC -/- MISCELLANEOUS: The C-terminal region is probably used for
 anchoring the protein to the cell membrane. The repeat sequences
 would be the surface antigen of the organism.
 CC -/- SIMILARITY: Contains 1 tsp type-1 domain.

SEQUENCE FROM N.A.
 MEDLINE=89364938; PubMed=2671723;
 RX Caspers P., Ganz T.R., Matile H., Pink J.R., Sinigaglia F.;
 RA "The circumsporozoite protein gene from NF54, a Plasmodium falciparum
 isolate used in malaria vaccine trials."
 RT Mol. Biochem. Parasitol. 35:185-190 (1989)./
 RL -/- FUNCTION: The circumsporozoite protein is the immunodominant
 surface antigen on the sporozoite (the infective stage of the
 malaria parasite that is transmitted from the mosquito to the
 vertebrate host).
 CC -/- MISCELLANEOUS: The C-terminal region is probably used for
 anchoring the protein to the cell membrane. The repeat sequences
 would be the surface antigen of the organism.
 CC -/- SIMILARITY: Contains 1 tsp type-1 domain.

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REPEAT REPEAT 148 151
 REPEAT 152 155 9.
 REPEAT 156 159 10.
 REPEAT 160 163 11.
 REPEAT 164 167 12.
 REPEAT 168 171 13.
 REPEAT 172 175 14.
 REPEAT 176 179 15.
 REPEAT 180 183 16.
 REPEAT 184 187 17.
 REPEAT 188 191 18.
 REPEAT 192 195 20.
 REPEAT 196 199 21.
 REPEAT 200 203 22.
 REPEAT 204 207 23.
 REPEAT 208 211 24.
 REPEAT 212 215 25.
 REPEAT 216 219 26.
 REPEAT 220 223 27.
 REPEAT 224 227 28.
 REPEAT 228 231 29.
 REPEAT 232 235 30.
 REPEAT 236 239 31.
 REPEAT 240 243 32.
 REPEAT 244 247 33.
 REPEAT 248 251 34.
 REPEAT 252 255 35.
 REPEAT 256 259 36.
 REPEAT 260 263 37.
 DOMAIN 313 366 TSP TYPE-1.
 SEQUENCE 388 AA; 42245 MW; CO31BEE2E35604 CRC64;

Query Match Score 97; DB 1; Length 388;
 Best Local Similarity 53.0%; Pred. No. 4.3e-06;
 Matches 22; Conservative 3; Mismatches 5; Indels 1;
 Gaps 8; Signal 1;

REPEAT 7 LRPGSGGPSLD-----EKKIAKMEKASSVFNVNNS 36
 Db 337 IKGAGKPKDQDYNDLEKKICRNEKCSSVFNVNNS 374

RESULT 2
 CSP_PLAFO STANDARD: PRT; 397 AA.
 ID _CSP_PLAFO
 AC P193597; Q25798;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DB Circumsporozoite protein Precursor (CS).
 OS Plasmodium falciparum (isolate NF54).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TAXID=5843;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=8945189; PubMed=2668895;
 RX Campbell J.R.;
 RX "DNA sequence of the gene encoding a Plasmodium falciparum malaria
 candidate vaccine antigen,";
 RT Nucleic Acids Res. 17:5851-5854 (1989).
 RN [2]
 RP REVISIONS.
 RP Campbell J.R.;
 RP Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9215298; PubMed=1346766;
 RA Davis J.R., Cortese J.F., Herrington D.A., Murphy J.R., Clyde D.F.,
 RA Thomas A.W., Baier S., Cochran M.A., Thalasssi J., Levine M.M.,
 RA Hackett C.S.;
 RA "Plasmodium falciparum: in vitro characterization and human
 RY infectivity of a cloned line.";
 RY Exp. Parasitol. 74:159-168 (1992).
 RP [4]

RESULT 3
 ID - CSP_PLAFA STANDARD; PRT; 412 AA.
 AC P02693;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84250215; PubMed=6204383;
 RA Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Witz R.A.,
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DB Circumsporozoite Protein Precursor (CS).
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TAXID=5833;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=84250215; PubMed=6204383;
 RA Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Witz R.A.,
 RA Hochmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
 RA Sanders G.S., Reddy E.P., Diggs C.L., Miller L.H.;
 RT Structure of the gene encoding the immunodominant surface antigen on
 the sporozoite of the human malaria parasite Plasmodium falciparum.;
 RL Science 225:593-599(1984)
 :- FUNCTION: The circumsporozoite protein is the immunodominant
 surface antigen on the sporozoite (the infective stage of the
 malaria parasite that is transmitted from the mosquito to the
 vertebrate host).
 :- MISCELLANEOUS: The C-terminal region is probably used for
 anchoring the protein to the cell membrane. The repeat sequences
 would be the surface antigen of the organism.
 :- SIMILARITY: Contains 1 TSP type 1 domain.

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 CC use by non-profit institutions that are not removed. Usage by and for commercial
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to licenses@isb-sib.ch).
 CC
 DR EMBL; K02194; AA129524.1; -
 DR InterPro; IP000367; Crcmsprzoite.
 DR InterPro; IP0003684; TSP1.
 DR Pfam; PF00094; tsp1.
 DR PRINTS; PR01303; CRCMSPRZOITE.
 DR SMART; SM00029; TSP1; 1.
 DR PROSITE; PS50092; TSP1; 1.
 DR Malaria; Sporozoite; Repeat; Signal.
 KW SIGNAL 1 16 PROBABIL.
 FT CHAIN 17 412 CIRCUMSPOROZOITE PROTEIN.
 FT DOMAIN 123 286 41 X 4 AA TANDEM REPEATS OF P-N-[AV]-[ND].
 FT REPEAT 123 126 1.
 FT REPEAT 127 130 2.
 FT REPEAT 131 134 3.

RESULT 4
 ID - CSP_PLAFT STANDARD; PRT; 424 AA.
 AC P13814;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-2004 (Rel. 13, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DB Circumsporozoite protein precursor (CS).
 OS Plasmodium falciparum (isolate t4 / Thailand)
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TAXID=5846;
 RN [1]
 SEQUENCE FROM N.A.
 RP MEDLINE=9731205; PubMed=3306373;
 RX ID - CSP_PLAFT
 RA del Portillo H.A., Nussenzweig R.S., Enea V.;
 RT "Circumsporozoite gene of a Plasmodium falciparum strain from Thailand.";
 RT Mol. Biochem. Parasitol. 24:289-294 (1987).
 CC -!- FUNCTION: The circumsporozoite protein is the immunodominant
 CC surface antigen that is transmitted from the mosquito to the
 CC malaria parasite that is transmitted from the mosquito to the
 CC vertebrate host).
 CC -!- MISCELLANEOUS: The C-terminal region is probably used for

Query 7 LRPGSSGPSDL-----EKXTAKMKEKASSVENVNS 36
 SQ :|||:|||||:|||||:|||||:|||||:|||||:|||||:
 Query Match 49.7% Score 91; DB 1; Length 412;
 Best Local Similarity 55.3%; Pred. No. 3.3e-05;
 Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;
 Db 361 IKPSANKPKDDEYDIEKKICMKCSSVNVNS 398

anchoring the protein to the cell membrane. The repeat sequences would be the surface antigen of the organism.

-|- SIMILARITY: Contains 1 TSP type-1 domain.

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CC DR EMBL; M19752; AA29555.1.
 CC DR A54533; A54533; Crcmsprzoite.
 CC DR InterPro; IPR003667; Crcmsprzoite.
 CC DR InterPro; IPR000894; TSPI1.
 CC DR PRINTS; PRO1303; TSP1; 1.
 CC DR SMART; SM00209; TSPI1; 1.
 CC DR PROSITE; PSS0092; TSPI1; 1.
 KW Malaria; Sporozoite; Repeat; Signal.
 FT SIGNAL 1 16 PROBABLE.
 FT CHAIN 17 424 CIRCUMSPOROZOITE PROTEIN.
 FT DOMAIN 123 298 44 X₄ AA TANDEM REPEATS OF P-N-[AV]-
 FT PT REPEAT 123 126 1.
 FT PT REPEAT 127 130 2.
 FT PT REPEAT 131 134 3.
 FT PT REPEAT 135 138 4.
 FT PT REPEAT 139 142 5.
 FT PT REPEAT 143 146 6.
 FT PT REPEAT 147 150 7.
 FT PT REPEAT 151 154 8.
 FT PT REPEAT 155 158 9.
 FT PT REPEAT 159 162 10.
 FT PT REPEAT 163 166 11.
 FT PT REPEAT 167 170 12.
 FT PT REPEAT 171 174 13.
 FT PT REPEAT 175 178 14.
 FT PT REPEAT 179 182 15.
 FT PT REPEAT 183 186 16.
 FT PT REPEAT 187 190 17.
 FT PT REPEAT 191 194 18.
 FT PT REPEAT 195 198 19.
 FT PT REPEAT 199 202 20.
 FT PT REPEAT 203 206 21.
 FT PT REPEAT 207 210 22.
 FT PT REPEAT 211 214 23.
 FT PT REPEAT 215 218 24.
 FT PT REPEAT 219 222 25.
 FT PT REPEAT 223 226 26.
 FT PT REPEAT 227 230 27.
 FT PT REPEAT 231 234 28.
 FT PT REPEAT 235 239 29.
 FT PT REPEAT 239 242 30.
 FT PT REPEAT 243 246 31.
 FT PT REPEAT 247 250 32.
 FT PT REPEAT 251 254 33.
 FT PT REPEAT 255 258 34.
 FT PT REPEAT 259 262 35.
 FT PT REPEAT 263 266 36.
 FT PT REPEAT 267 270 37.
 FT PT REPEAT 271 274 38.
 FT PT REPEAT 275 278 39.
 FT PT REPEAT 279 282 40.
 FT PT REPEAT 283 286 41.
 FT PT REPEAT 287 290 42.
 FT PT REPEAT 291 294 43.
 FT PT REPEAT 295 298 44.
 FT DOMAIN 349 402 TSP TYPE-1.
 SQ SEQUENCE 424 AA; 45610 MW; 710AB14238786CD9 CRC64;
 SQ Score 91; DB 1; Length 424;

Best Local Similarity	55.3%	Pred. No.	3.4e-05	;
Matches	21	Conservative	3	Mismatches
Indels	6	Gaps	8	1;
Qy	7 LRPGSGPSLID-----EKKIAKEKASSVENVNVS	36		
Db	373 TREGSANKPKDLDYNDIEKICKMEKCSSVENVNVS	410		
RESULT 5				
ID	CSP_PLAFW	STANDARD;	PRT;	442 AA.
AC	PO5307;			
DT	01-AUG-1988 (Rel. 08, Last sequence update)			
DT	01-AUG-1988 (Rel. 43, Last annotation update)			
DE	Circumsporozoite protein precursor (CS).			
OS	Plasmodium falciparum (issolate Wellcome)			
OC	Bukaryota; Alveorata; Apicomplexa;			
NCBI_TAXID	5848;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-87115616; PubMed=2543671;			
RA	LOCKYER M.J.; Schwarz R.T.;			
RT	"Strain variation in the circumsporozoite protein gene of Plasmodium falciparum."			
RT	Parasitol. 22:101-108(1987).			
RL	Mol. Biochem.			
CC	- - FUNCTION: The circumsporozoite protein is the immunodominant surface antigen on the sporozoite (the infective stage of the mosquito to the vertebrate host).			
CC	- - MISCELLANEOUS: The C-terminal region is probably used for anchoring the protein to the cell membrane. The repeat sequences would be the surface antigen of the organism.			
CC	- - SIMILARITY: Contains 1 TSP type-1 domain.			
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CC	CC			
DR	EMBL; M15505; AAA29554.1; -.			
DR	PIR; A54529; A54529.			
DR	InterPro; IPR0306; Crcmsprzoite.			
DR	InterPro; IPR00884; TSPI1.			
DR	Pfam; PF00090; tsp1; 1.			
DR	PRINTS; PR01303; CRCMSPRZOITE.			
DR	SMART; SM00209; TSPI1; 1.			
DR	PROSITE; PS50092; TSPI1; 1.			
KW	Malaria; Sporozoite; Repeat; Signal.			
FT	SIGNAL 1 16 CIRCUMSPOROZOITE PROTEIN.			
FT	CHAIN 17 442 CIRCUMSPOROZOITE PROTEIN.			
FT	DOMAIN 134 317 46 X 4 AA TANDEM REPEATS OF P-N-[AV]-[IND]-P.			
FT	REPEAT 134 137 1.			
FT	REPEAT 138 141 2.			
FT	REPEAT 142 145 3.			
FT	REPEAT 146 149 4.			
FT	REPEAT 150 153 5.			
FT	REPEAT 154 157 6.			
FT	REPEAT 158 161 7.			
FT	REPEAT 162 165 8.			
FT	REPEAT 166 169 9.			
FT	REPEAT 170 173 10.			
FT	REPEAT 174 177 11.			
FT	REPEAT 178 181 12.			
FT	REPEAT 182 185 13.			
FT	REPEAT 186 189 14.			
FT	REPEAT 190 193 15.			
FT	REPEAT 194 197 16.			
FT	REPEAT 198 201 17.			

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CC   EMBL; U91938; AAB51302; 1;
CC   InterPro; IPR002012; GRNH.
CC   Pfam; PRO0446; GRNH; 1.
CC   PRANTS; PRO15161; GONADOLIBRN1.
CC   PROSITE; PS00473; GRNH; 1.
CC   Cleaveage on pair of basic residues; Hormone; Amidation; Hypothalamus;
KW   Placenta; Pyrrolidone carboxylic acid.
KW
FT  NON_TER    1      1
FT  PT          1      >63  PROGONADOLIBERIN I.
FT  CHAIN      1      10   GONADOLIBERIN I.
FT  PEPTIDE     1      >63  GRNH-ASSOCIATED PEPTIDE I (BY
FT  PEPTIDE     14      SIMILARITY)
FT  ACT_SITE    3      3   SIMILARITY) * ESSENTIAL FOR BIOLOGICAL
FT          ACTIVITY (BY SIMILARITY).
FT  MOD_RES     1      1   PYRROLIDONE CARBOXYLIC ACID (BY
FT          SIMILARITY)
FT  MOD_RES     10     10   AMIDATION (G-11 PROVIDE AMIDE GROUP) (BY
FT          SIMILARITY).
FT  NON_TER    63      63  FC94995676F77180 CRC64;
SQ  SEQUENCE    63 AA; 7370 MW;
Query Match 32.2%; Score 59; DB 1; Length 63;
Best Local Similarity 52.2%; Pred. No. 0.14;
Matches 12; Conservative 0; Mismatches 5; Indels 6; Gaps 1;
Qy  2 HWSYGLRPQSS-----GSLSLDE 18
Db  2 HWSYGLRPQGGKRNAAERLGDSFQE 24

```

RESULT 8

GONI_MACMU	STANDARD;	PRTR;	67 AA.
ID P5527;			
AC DT 01-OCT-1996 (Rel. 34, Created)			
DT 01-OCT-1986 (Rel. 34, Last sequence update)			
DT 28-FEB-2003 (Rel. 41, Last annotation update)			
DB Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)]			
DE Luteinizing hormone-releasing hormone I (Gonadotropin-releasing hormone I) (GRNH I) (Lliberin II); GRNH-associated peptide II (Fragment).			
DE (FRAGMENT).			
OS Macaca mulatta (Rhesus macaque).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC Mammalia; Butheria; Primates; Catarrhini; Cercopithecoidea;			
OC Cercopithecinae; Macaca.			
NCBI_TaxID=9544;			
RN [1]			
SEQUENCE FROM N.A.			
RC TISSUE:Hypothalamus;			
RC MEDLINE=951124501; PubMed=7545971;			
RA Ma Y.-J.; Costa M.B.; Ojea S.R.;			
RT "Developmental expression of the genes encoding transforming growth factor alpha and its receptor in the hypothalamus of female rhesus macaques."			
RT Neuroendocrinology 60:346-359 (1994).			
RL CC -I- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.			
CC -I- SUBCELLULAR LOCATION: Secreted.			
CC -I- SIMILARITY: Belongs to the GRNH family.			
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CC	EMBL: S75918; AA533 095-1; -.
DR	PTR: I18541; I78541;
DR	InterPro; IPR02011; GGRH,
DR	InterPro; IPR004079; GonadoliberinI.
DR	PFam: PF00446; GRH; 1.
PRINTS; PR01541; GONADOLIBERNI.	
DR	PROSITE; PS00473; GRNH; 1.
KW	Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
KW	Signal; Pyrrolidone carboxylic acid.
FT	NON_TER 1 1 BY SIMILARITY.
FT	SIGNAL <1 5 BY SIMILARITY.
FT	CHAIN 6 6 PROGONADOLIBERIN I.
FT	PEPTIDE 5 15 GONADOLIBERIN I.
FT	PEPTIDE 19 7 GNRH-ASSOCIATED PEPTIDE I.
ACT_SITE	8 8 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
FT	ACTIVITY (BY SIMILARITY).
FT	MOD_RES 6 6 PYRROLIDONE CARBOXYLIC ACID (BY
FT	SIMILARITY).
FT	AMIDATION (G-16 PROVIDE AMIDE GROUP) (BY
FT	SIMILARITY).
FT	NON_TER 15 15
FT	SEQUENCE 67 67 AA; 7573 MW; 505394DA261A3F2 CRC64;
SQ	Query Match 31.7%; Score 56; DB 1; Length 67;
	Best Local Similarity 100.0%; Prd. No. 0.21;
	Mismatches 0; Indels 0; Caps
Qy	2 HWSYGLRP 10
Db	7 HWSYGLRP 15

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RESULT 9
GONI-XENIA
ID - GONI-XENIA      STANDARD;          PRT;      89 AA.
AC P45556;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadotropin precursor (Gonadotropin-releasing hormone I) (GnRH-I)
DE (LH-EH) Nulliberlin I.
OS Xenopus laevis (African clawed frog).
OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopoda; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Forebrain; PubMed=8137750;
RX MEDLINE=94185563;
RA Hayes W.P., Wray S., Battley J.F. ;
RT "The frog Gonadotropin-releasing hormone-I (GnRH-I) gene has a
mammalian-like expression pattern and conserved domains in
GnRH-associated peptide, but brain onset is delayed until
metamorphosis." ;
RT Endocrinology 134:1835-1844 (1994).
RL Endocrinology 134:1835-1844 (1994).
CC [-] FUNCTION: Stimulates the secretion of gonadotropins.
CC [-] SUBCELLULAR LOCATION: Secreted.
CC [-] SIMILARITY: Belongs to the GnRH family.
CC
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/gonadoliberini/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; L28040; AAA49728.1;
DR PIR; I514423; T51423;
DR InterPro; IPR002012; GnRH;
DR InterPro; IPR004079; Gonadoliberini_I.

```


RX MEDLINE=99318093; PubMed=10391209;
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
 Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 Lander E.S.;
 RT "Characterization of single-nucleotide polymorphisms in coding regions
 of human genes";
 RT Nat. Genet. 22:231-238(1999).
 [6]
 RP ERRATUM.
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
 Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 Lander E.S.;
 RA FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 the secretion of both luteinizing and follicle-stimulating
 hormones.
 CC -!- PHARMACEUTICAL: Available under the names Factrel (Ayerst Labs),
 Latrepulse or Lutrelelf (Ferring Pharmaceuticals) and Reliborn
 (Serono).
 CC -!- SIMILARITY: Belongs to the GnRH family.
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 CC DR EMBL; X01059; CAA25226.1; -;
 DR GO; GO:0005183; F: luteinizing hormone-releasing factor activity; TAS.
 DR GO; GO:0007267; P: cell-cell signaling; TAS.
 DR GO; GO:0007275; P: development; TAS.
 DR GO; GO:0008285; P: negative regulation of cell proliferation; TAS.
 DR Gene; HGNC:4419; GNRHL.
 DR MIM: 152700; -;
 DR GO; GO:000625; C: soluble fraction; TAS.
 DR GO; GO:0005183; F: luteinizing hormone-releasing factor activity; TAS.
 DR GO; GO:0007267; P: cell-cell signaling; TAS.
 DR GO; GO:0007275; P: development; TAS.
 DR GO; GO:0007165; P: signal transduction; TAS.
 DR InterPro; IPR00212; GnRH.
 DR InterPro; IPR004079; Gonadotropin.
 DR PRINTS; PR01541; GONADOLIBRNI.
 DR PROSITE; PS00473; GnRH_1.
 DR Placenta; Placenta.
 KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 KW Placenta; Pharmaceutical; Signal; Polymorphism;
 KW Pyrrolidone carboxylic acid.
 FT SIGNAL 1 23 PROGNODOLIBERIN I.
 FT CHAIN 24 92 GONADOLIBERIN I.
 FT PEPTIDE 24 33 GNRH-ASSOCIATED PEPTIDE I.
 FT PEPTIDE 37 92 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
 FT ACT SITE 26 26 ACTIVITY.
 FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
 FT VARIANT 16 16 W -> S (in dbSNP: 6185).
 FT /FTID:VAR_013943.
 SQ SEQUENCE 92 AA; 10380 MW; 30A/22218076FA79 CRC64;

Query Match 31.7%; Score 58; DB 1; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Coy 2 HWSYGLRPG 10
 Dbl 25 HWSYGLRPG 33

RESULT 14
 GON1_RAT STANDARD: PRT;
 ID GON1_RAT
 AC P07450;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Progonadotropin I precursor (Contains: Gonadotropin I (LH-RH I))
 DE (Luteinizing hormone-releasing hormone I) (Gonadotropin I (LH-RH I))
 DE (hormone I) (GnRH I); Prolactin release-inhibiting factor
 DE I.;
 DE GNRH1 OR GNRH;
 RN Rat norvegicus (Rat);
 OC Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteraria; Rodentia; Sciurognathi; Murinae; Rattus.
 NCBI_TaxId10116;
 RN [1];
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86094338; PubMed=2867548;
 RA Adelman J.P., Mason A.J., Haylick J.S., Seburg P.H.;
 RT "Isolation of the gene and hypothalamic cDNA for the common precursor
 of gonadotropin-releasing hormone and prolactin release-inhibiting
 factor in human and rat";
 RT Proc. Natl. Acad. Sci. U.S.A. 83:179-183(1986).
 RN [2];
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83384661; PubMed=2476669;
 RA Bond C.T., Haylick J.S., Seburg P.H., Adelman J.P.;
 RT "Thymocytes express a mRNA that is identical to hypothalamic
 luteinizing hormone-releasing hormone mRNA.";
 RT Mol. Endocrinol. 3:1257-1262 (1989).
 RN [3];
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE=93105480; PubMed=1468115;
 RA Maier C.C., Marchetti B., Leboeuf R.D., Blalock J.E./
 RT "The rat Gonadotropin-releasing hormone: SH locus: structure and
 hypothalamic expression";
 RT Mol. Endocrinol. 3:1257-1262 (1989).
 RN [4];
 RP SEQUENCE OF 1-47 FROM N.A.
 RP TISSUE=Heart;
 RX MEDLINE=87149087; PubMed=3547652;
 RA Adelman J.P., Bond C.T., Douglass J., Herbert E.;
 RT "Two mammalian genes transcribed from opposite strands of the same
 DNA locus";
 RT Science 235:1514-1517(1987).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Central nervous system.
 CC -!- SIMILARITY: Belongs to the GnRH family.

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 CC or send an email to license@isb-sib.ch).
 CC -!- DR EMBL; S50870; AAB24572.1; -;
 CC -!- DR EMBL; M12579; AAA41263.1; -;
 CC -!- DR EMBL; M31670; AAA41264.1; -;
 CC -!- DR EMBL; M15527; AAA21241.1; ALT_SEQ.
 CC -!- DR EMBL; M15523; AAA42339.1; -;
 CC -!- DR EMBL; M15526; -; NOT_ANNOTATED_CDS.
 CC -!- DR PIR; A40147; RHTG.
 DR InterPro; IPR00212; GnRH.
 DR InterPro; IPR004079; Gonadotropin.
 DR Pfam; PF00446; GnRH_1.
 DR PRINTS; PRO1541; GONADOLIBRNI.

DR PROSITE; PS00473; GNRH; 1.
 KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 KW Placenta; Signal; Pyrroldione carboxylic acid.
 FT SIGNAL 1 23
 FT CHAIN 24 92 PROGNADOLIBERIN I.
 PT PEPTIDE 24 33 GONADOLIBERIN I.
 PT PEPTIDE 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
 ACT_SITE 26 26 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
 ACTIVITY.
 FT MOD_RBS 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
 AMIDATION (G-34 PROVIDE AMIDE GROUP) (BY
 SIMILARITY).
 FT SQ SEQUENCE 92 AA; 10197 MW; 4FDDB2C50CF5F63B CRC64;
 FT Query Match 31.7%; Score 58; DB 1; Length 92;
 FT Best Local Similarity 100.0%; Pred. No. 0.3;
 FT Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 FT
 SQ 92 AA; 10500 MW;
 494B5C64DA8A3EB3 CRC64;
 FT
 Query Match 31.7%; Score 58; DB 1; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 FT
 Job completed: March 10, 2004, 09:13:57
 Job time : 6.5836 secs

RESULT 15
 GONI_TURGB STANDARD: PRT: 92 AA.
 AC Q93J5;
 AC ID_GONI_TURGB
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DB Gonadotropin I Precursor [Contains: Gonadotropin I (LH-RH I)
 DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
 hormone I) (GnRH I); Lulliberin I; GnRH-associated peptide I].
 DE (GnRH I) (GnRH II) (GnRH III); GnRH.
 OS Tupaia glis belangeri (Common tree shrew).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Scandentia; Tupaidae; Tupaia.
 OX NCBI_TAXID=3347;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=hypothalamus;
 RA MEDLINE=97079639; PubMed=8921350;
 RA Kasten T.L., White S.A., Norton T.T., Bond C.T., Adelman J.P.,
 RA Fernald R.D.;
 RA "Characterization of two new preproGnRH mRNAs in the tree shrew: a first direct evidence for mesencephalic GnRH gene expression in a placental mammal".
 RA Comp. Endocrinol. 104:7-19 (1996).
 RL -!- FUNCTION: Stimulates the secretion of Gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GnRH family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 EMBL: U63126; AAB1837.1;
 DR InterPro; IPR002012; GnRH
 DR InterPro; IPR04079; Gonadoliberin I.
 DR Pfam; PF00446; GnRH; 1.
 PRINTS; PRO1541; GONADOLIBERNI.
 DR PROSITE; PS00473; GnRH; 1.
 RW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 RW Placenta; Signal; Pyrrolidone carboxylic acid.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT CHAIN 24 92 PROGNADOLIBERIN I.
 FT PEPTIDE 24 33 GONADOLIBERIN I.
 FT PEPTIDE 37 92 GNRH-ASSOCIATED PEPTIDE I.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 35.5798 Seconds
(without alignments)
319.245 Million cell updates/sec

Title: US-09-848-834A-16

Perfect Score: 183

Sequence: 1 XHNSYGLRPSSGPSLDEKKIAKMEKASSVENTVNS 36

Scoring table: BLOSSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

SPTREMBL 25:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	55.7	117	5 Q25797	Q25797 Plasmodium
2	102	55.7	408	5 Q25729	Q25729 Plasmodium
3	102	55.7	436	5 Q27325	Q27325 Plasmodium
4	98	53.6	79	5 Q9u0g2	Q9u0g2 Plasmodium
5	98	53.6	392	5 Q8i9h8	Q8i9h8 Plasmodium
6	98	53.6	396	5 Q8i111	Q8i111 Plasmodium
7	98	53.6	395	5 Q8i9j0	Q8i9j0 Plasmodium
8	98	53.6	396	5 Q8i9h9	Q8i9h9 Plasmodium
9	97	53.0	360	5 Q8i9h7	Q8i9h7 Plasmodium
10	97	53.0	360	5 Q8i9h6	Q8i9h6 Plasmodium
11	97	53.0	412	5 Q8i9h5	Q8i9h5 Plasmodium
12	97	53.0	420	5 Q258318	Q258318 Plasmodium
13	94	51.4	389	5 Q8i9j2	Q8i9j2 Plasmodium
14	94	51.4	393	5 Q8i1j1	Q8i1j1 Plasmodium
15	91	49.7	69	5 Q8M9K7	Q8M9K7 Plasmodium
16	91	49.7	80	5 Q9u0p3	Q9u0p3 Plasmodium

ALIGNMENTS

RESULT 1	Q25797	PRELIMINARY;	PRT;	117 AA.
ID	Q25797			
AC	Q25797;			
DT	01-NOV-1996 (TrEMBLrel 01, Created)			
DT	01-OCT-2000 (TrEMBLrel 15, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel 24, Last annotation update)			
DB	Circumsporozoite protein (Fragment).			
OS	Plasmodium falciparum.			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.			
OX				
RN	[1]; NCBI_TaxID=533;			
RP				
SEQUENCE FROM N.A.				
RA	Doolan D.L., Saul A., Good M.F.			
RT	"Geographically restricted heterogeneity of the Plasmodium falciparum circumsporozoite protein: relevance for vaccine development."			
RL	Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; M77205; AA29519; 2;			
GO	GO:0003793; F: defense/immunity protein activity; IFA.			
DR	InterPro; IPR003067; CRCmsprzoite.			
DR	InterPro; IPR000864; TSP1.			
DR	Pfam; PF00097; tspl_1.			
DR	PRINTS; PRO103; CRCMSPRZOITE.			
DR	SMART; SM00299; TSPL1.			
DR	PROSITE; PSS0092; TSP1.			
FT				
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FT				
SQ	SEQUENCE 117 AA, 13043 MW, ODA711D86COB03C1 CRC64;			
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DR	PRINTS; PRO103; CRCMSPRZOITE.			
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DR	PROSITE; PSS0092; TSP1.			
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DR	PROSITE; PSS0092; TSP1.			
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DR	PROSITE; PSS0092; TSP1.			
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NON_TER	1			
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SQ	SEQUENCE 117 AA, 13043 MW, ODA711D86COB03C1 CRC64;			
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NON_TER	1			
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DR	PROSITE; PSS0092; TSP1.			
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NON_TER	1			
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SQ	SEQUENCE 117 AA, 13043 MW, ODA711D86COB03C1 CRC64;			
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DR	PROSITE; PSS0092; TSP1.			
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NON_TER	1			
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DR	PROSITE; PSS0092; TSP1.			
FT				
NON_TER	1			
FT				
SQ	SEQUENCE 117 AA, 13043 MW, ODA711D86COB03C1 CRC64;			
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DR	SMART; SM00299; TSPL1.			
DR	PROSITE; PSS0092; TSP1.			
FT				
NON_TER	1			
FT				
SQ	SEQUENCE 117 AA, 13043 MW, ODA711D86COB03C1 CRC64;			
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DR	PRINTS; PRO103; CRCMSPRZOITE.			
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DR	PROSITE; PSS0092; TSP1.			
FT				
NON_TER	1			
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DR	PROSITE; PSS0092; TSP1.			
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DR	PROSITE; PSS0092; TSP1.			
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NON_TER	1			
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DR	PROSITE; PSS0092; TSP1.			
FT				
NON_TER	1			
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SQ	SEQUENCE 117 AA, 13043 MW, ODA711D86COB03C1 CRC64;			
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DR	PRINTS; PRO103; CRCMSPRZOITE.			
DR	SMART; SM00299; TSPL1.			
DR	PROSITE; PSS0092; TSP1.			
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SQ	SEQUENCE 117 AA, 13043 MW, ODA711D86COB03C1 CRC64;			
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DR	SMART; SM00299; TSPL1.			
DR	PROSITE; PSS0092; TSP1.			
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NON_TER	1			
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SQ	SEQUENCE 117 AA, 13043 MW, ODA711D86COB03C1 CRC64;			
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NON_TER	1			
FT				
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NON_TER	1			
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DR	SMART; SM00299; TSPL1.			
DR	PROSITE; PSS0092; TSP1.			</td

Q25729 PRELIMINARY; PRT; 408 AA.
 ID Q25729; PRELIMINARY; PRT; 408 AA.
 AC Created)
 DR 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DR 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Circumsporozoite protein.
 CN CS
 OS Plasmodium falciparum; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OC NCBI_TaxID=833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Santa Lucia;
 RA Qari S.H., Lal A.A.; Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U20969; AA63155..1; -.
 DR GO:0000373; F:defense,immunity protein activity; IEA.
 DR InterPro; IPR003667; Crcmbsrzoite.
 DR InterPro; IPR000884; TSP1.
 DR PRINTS; PRO1303; CRCMSPRZOITE.
 DR SMART; SM0209; TSP1; 1.
 DR PROSITE; PS50092; TSP1; 1.
 KW Malaria.
 SQ 408 AA; 43871 MW; A545BE517822515C CRC64;
 SEQUENCE 55.7%; Score 102; DB 5; Length 408;
 Best Local Similarity 60.5%; Pred. No. 4.3e-06;
 Matches 23; Conservative 3; Mismatches 4; Indels 8; Gaps 1;
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=837;
 RA la Cruz V.F.; Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=837;
 RA Jochimtives, S., Tanabe K., Kanbara H.; Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; MB3164; AAA2542..1; -.
 DR EMBL; MB3150; AAA25563..1; -.
 DR EMBL; MB3163; AAA2357..1; -.
 DR GO:0003793; F:defense,immunity protein activity; IEA.
 DR InterPro; IPR003667; Crcmbsrzoite.

DR InterPro; IPR000884; TSP1.
 DR PRINTS; PRO1303; CRCMSPRZOITE.
 DR SMART; SM00209; TSP1; 1.
 DR PROSITE; PS50092; TSP1; 1.
 FT NON TER 1
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 SQ 53.6%; Score 98; DB 5; Length 79;
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 Matches 22; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

Q81958 PRELIMINARY; PRT; 392 AA.
 ID Q81958; PRELIMINARY; PRT; 392 AA.
 AC Created)
 DR 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DR PRINTS; PRO1303 (TREMBLrel. 24, Last annotation update)
 DE Circumsporozoite protein.
 CN CS
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Asemblo Bay; MEDLINE=22356746; PubMed=12467976;

RESULT	SQ	SEQUENCE	360 AA;	39062 MW;	65058844270D66C CRC64;
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	AC	Q819H7;	SEQUENCE FROM N.A.		
	DR	01-MAR-2003 (TREMBLrel. 23; Created)			
	DR	01-MAR-2003 (TREMBLrel. 23; Last sequence update)			
	DR	01-JUN-2003 (TREMBLrel. 24; Last annotation update)			
	DE	Circumsporozoite protein.			
	GN	CSP.			
	OS	Plasmodium falciparum.			
	OC	Eukaryote; Alveolata; Apicomplexa; Haemosporida; Plasmodium.			
	OX	NCBI_TaxID=5833;			
	RN	[1]			
	RP	SEQUENCE FROM N.A.			
	RC	STRAIN Asumbo Bay;			
	RD	MEDLINE=22316746; PubMed=12467976;			
	RX	InterPro; IPRO003793; F-defense/immunity protein activity; IEA.			
	RA	Escalante A.A., Grebert H.M., Isea R., Goldman I.F., Basco L., Magris M., Biswas S., Kariuki S., Lal A.A.; "A study of genetic diversity in the gene encoding the circumsporozoite protein (CSP) of Plasmodium falciparum from different transmission areas-XVI. Asumbo Bay Cohort Project.";			
	RT	Mol. Biochem. Parasitol. 125:83-90 (2002).			
	RT	InterPro; IPRO040462; AN87596.1;			
	DR	PRINTS; PRO1303; CRMSPRZTOITE.			
	DR	InterPro; IPRO00367; CRMSPRZTOITE.			
	DR	InterPro; IPRO00884; TSP1.			
	DR	PRINTS; PRO0092; TSP1; 1.			
	DR	PROSITE; PS50092; TSP1; 1.			
	DR	SEQUENCE 360 AA; 39093 MW; 6504CC012649236C CRC64;			
	DR	Query Match Score 97; DB 5; Length 360;			
	DR	Best Local Similarity 57.0%; Pred. Nc. 2e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
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	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	309 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 346			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
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	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
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	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
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	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
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	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
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	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
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	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
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	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
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	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			
	DR	361 IKPGSAGKPKDELDDYANDIEKKIAKMEKASSVENVNS 398			
	DR	Query Match Score 97; DB 5; Length 412;			
	DR	Best Local Similarity 57.9%; Pred. Nc. 2.3e-05;			
	DR	Matches 22; Conservative 3; Mismatches 5; Indels 8; Gaps 1;			
	DR	DE Circumsporozoite protein.			
	DR	RESULTS			
	DR	7 LRPGSSGSLD-----EKKIAKMEKASSVENVNS 36			

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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:48 ; Search time 54.2101 Seconds
 (without alignments)

Title: US-09-848-834A-16

Perfect score: 183

Sequence: 1 XHWNSYGLRPSSGGPSLDEKKIARMEKASSVENVNNS 36

Scoring table: BLASTM62

Gapp 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match %

Maximum Match %

Listing first 45 summaries

Result No.	Score	Query	Match	Length	DB ID	Description	Location/Qualifiers
1	182	99.5	36	5	AAU11427	Aau11427 Synthetic	FT Peptide 1..10 /note= "Gonadotrophin releasing hormone epitope"
2	182	99.5	51	5	AAU11431	Aau11431 Synthetic	FT Misc-difference 1 /label= OTHER
3	95	51.9	20	5	AAU11414	Aau11414 P. falcip	FT /note= "Other= Pyro-glutamic acid or 5-oxo proline"
4	95	51.9	33	5	AAU11433	Aau11433 Synthetic	FT Peptide 11..16 /note= "Spacer peptide"
5	91	49.7	309	2	AAU13175	Aar13175 NS1-81-RL	FT Peptide 17..36 /note= "Malaria CSP protein (378-398 aa)"
6	91	49.7	319	2	AAU0945	Aar0945 NS1-81-RL	FT Peptide 2000000000..2000000000 /note= "Malaria CSP protein (378-398 aa)"
7	91	49.7	319	2	AAU13176	Aar13176 NS1-81-RL	XX WO200185763-A2.
8	91	49.7	327	2	AAU13177	Aar13177 NS1-81 (NA	XX
9	91	49.7	335	2	AAU13178	Aar13178 NS1-81 (NA	XX
10	91	49.7	335	2	AAU13179	Aar13179 NS1-81 (NA	XX
11	91	49.7	396	7	ABO23530	Abo23530 Plasmodiu	XX
12	91	49.7	411	1	AAU83144	Aau83144 Sequence	PD 15-NOV-2001.
13	91	49.7	424	2	AAU60416	Aap60416 CS protei	XX
14	91	49.7	424	2	AAR37797	Aar37797 RTS. Prot	PF 04-MAY-2001; 2001WO-US014363.
15	91	49.7	424	2	AAR37796	Aar37796 RTS. Prote	XX
16	89.5	48.9	33	4	AAG633663	Aag633663 Peptide C	PR 05-MAY-2000;
17	89.5	48.9	33	4	AAG633516	Aag633516 A. peptide	XX
18	89	48.6	19	4	AAM98951	Aam98951 Vaccine r	PA (APHT-) APHTON CORP.
19	89	48.6	21	1	AAP91504	Aap91504 Sequence	XX
20	89	48.6	21	2	AAR18920	Aar18920 Malaria C	PI Grimes S, Michaeli D, Stevens V.C;
21	89	48.6	21	2	AAR75955	Aar75955 P. falcip	XX DR
22	89	48.6	21	2	AAR70912	Aar70912 Malaria C	WPI; 2002-049440/06.
23	89	48.6	21	2	AAR82586	Aar82586 Plasmodiu	PT Novel synthetic immunogen for inducing immune response against
24	89	48.6	21	2	AAW05612	Aaw05612 Circumspon	PT gonadotropin releasing hormone, comprises fusion peptide having
25	89	48.6	21	2	Aaw35440	Aaw35440 T-cell st	

PT Promiscuous helper T-cell peptide epitope and immunomimic peptide epitope or its analog.
 PT XX
 PS Claim 11; Page 10; 43pp; English.
 XX
 CC The invention relates to a synthetic immunogen for inducing specific antibodies against gonadotropin releasing hormone (GnRH) also known as luteinising hormone releasing hormone, LHRH comprising a fusion peptide which comprises a promiscuous helper T cell peptide epitope and immunomimetic peptide epitope or its analogue. The synthetic immunogen is useful inducing an immune response against GnRH in an animal subject, and such as useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer), endometriosis, uterine fibroids, benign prostatic hypertrophy and prostate cancer. The immunogen is effective in eliciting high and specific anti-GnRH antibody titres. The present sequence is a synthetic immunogen of the invention
 XX
 Sequence 36 AA;
 SQ Query Match 99.5%; Score 182; DB 5; Length 36;
 Best Local Similarity 100.0%; Pred. No. 4-7e-19;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DE 2 HWSYGLRPSSGPSSLDKEKKIARNEKASSVENTVNS 36
 Db 2 HWSYGLRPSSGPSSLDKEKKIARNEKASSVENTVNS 36

RESULT 2
 AAU11431 standard; peptide; 51 AA.
 XX AAU11431;
 AC DT 12-MAR-2002 (first entry)
 XX DE Synthetic immunogen peptide 12.
 XX Gonadotrophin releasing hormone; GnRH; synthetic immunogen;
 KW luteinising hormone releasing hormone; LHRH; contraceptive;
 KW promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
 KW breast cancer; uterine cancer; gynaecological cancer; endometriosis;
 KW uterine fibroid; benign prostatic hypertrophy; prostate cancer.
 XX OS Plasmodium falciparum.
 OS Mammalia.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key Peptide 1..10
 /note= "Gonadotrophin releasing hormone epitope (1..10 aa)"
 FT Misc-difference 1 /label= OTHER
 /note= "Other= Pyro-glutamic acid or 5-oxo proline"
 FT Peptide 11..16
 /note= "Spacer peptide"
 FT Peptide 17..36
 /note= "Malaria CSP protein (378-398 aa)"
 FT Peptide 37..42
 /note= "Spacer peptide"
 FT Peptide 43..51
 /note= "Gonadotrophin releasing hormone epitope (2-10 aa)"
 FT Modified-site 51
 /note= "Amidated glycine or glycamide"

PP 04-MAY-2001; 2001WO-US014363.
 XX 05-MAY-2000; 2000US-0202328P.
 PS (APHT-) APHTON CORP.
 XX
 PI Grimes S, Michaeli D, Stevens VC;
 XX DR WPI; 2002-049440/06.
 XX
 CC Novel synthetic immunogen for inducing immune response against Gonadotropin releasing hormone, comprises fusion peptide having promiscuous helper T-cell peptide epitope and immunomimic peptide epitope or its analog.
 XX
 PS Claim 11; Page 12-13; 43pp; English.
 XX
 CC The invention relates to a synthetic immunogen for inducing specific antibodies against gonadotropin releasing hormone (GnRH) also known as luteinising hormone releasing hormone, LHRH comprising a fusion peptide which comprises a promiscuous helper T-cell peptide epitope and immunomimetic peptide epitope or its analogue. The synthetic immunogen is useful inducing an immune response against GnRH in an animal subject, and such as useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer), endometriosis, uterine fibroids, benign prostatic hypertrophy and prostate cancer. The immunogen is effective in eliciting high and specific anti-GnRH antibody titres. The present sequence is a synthetic immunogen of the invention
 XX
 Sequence 51 AA;
 SQ Query Match 99.5%; Score 182; DB 5; Length 51;
 Best Local Similarity 100.0%; Pred. No. 7.1e-19;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DE 2 HWSYGLRPSSGPSSLDKEKKIARNEKASSVENTVNS 36
 Db 2 HWSYGLRPSSGPSSLDKEKKIARNEKASSVENTVNS 36
 XX Sequence 51 AA;

RESULT 3
 AAU11414
 ID AAU11414 standard; peptide; 20 AA.
 XX AC AAU11414;
 XX DT 12-MAR-2002 (first entry)

P. falciparum circumsporozoite protein, CSP, peptide.
 XX
 KW Gonadotrophin releasing hormone; GnRH; synthetic immunogen;
 KW luteinising hormone releasing hormone; LHRH; contraceptive;
 KW promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
 KW breast cancer; uterine cancer; gynaecological cancer; endometriosis;
 KW uterine fibroid; benign prostatic hypertrophy; prostate cancer;
 KW circumsporozoite protein; CSP.
 XX OS Plasmodium falciparum.
 XX DN WO200185763-A2.
 XX PR 04-MAY-2001; 2001WO-US014363.
 XX PR 05-MAY-2000; 2000US-0202328P.
 XX PA (APHT-) APHTON CORP.
 XX PI Grimes S, Michaeli D, Stevens VC;
 XX DR WPI; 2002-049440/06.

XX 19-JUN-1991.
 PD 22-NOV-1990.
 XX XX
 PF 01-MAY-1990;
 PR 90EP-00304720.
 XX XX
 PR 01-MAY-1989;
 DR 89US-0034663.
 XX XX
 (SMK) SMITHKLINE BEECHAM.
 PA (USSA) US SBC OF ARMY.
 PA (BIOM- BIOMEDICAL RES INST.
 PA (GROS/) GROSS M. S.
 XX XX
 Gross MS, Young JF;
 PI WPI: 1990-350299/47.
 XX XX
 New polypeptide used in malaria vaccine - comprises immunogenic surface determinants from 1st and 2nd flanking regions of plasmodium surface protein and intermediate repeat domain.

PR Example 2: Page 11-12; 24pp; English.

PS The product is useful in preparation of vaccines for treatment and prevention of plasmodium sporozoite infection. It may be easily produced by polymeraxis of plasmodium sporozoite transformed E. coli expression system. (Updated on 25-MAR-2003 to correct PA field.)

CC The product is useful in preparation of vaccines for treatment and prevention of plasmodium sporozoite infection. It may be easily produced by polymeraxis of plasmodium sporozoite transformed E. coli expression system. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 319 AA;

Query Match 49.7%; Score 91; DB 2; Length 319;
 Best Local Similarity 55.3%; Prod. No. 0.00012;
 Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

CC Sequence 319 AA;

Query Match 49.7%; Score 91; DB 2; Length 319;
 Best Local Similarity 55.3%; Prod. No. 0.00012;
 Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

XX Sequence 319 AA;

Query Match 49.7%; Score 91; DB 2; Length 319;
 Best Local Similarity 55.3%; Prod. No. 0.00012;
 Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

CC Sequence 319 AA;

Query Match 49.7%; Score 91; DB 2; Length 319;
 Best Local Similarity 55.3%; Prod. No. 0.00012;
 Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

XX Sequence 319 AA;

RESULT 7 AARI3176 standard; protein; 319 AA.
 ID AARI3176 standard; protein; 319 AA.
 XX XX
 AC AARI3176;
 XX XX
 DT 24-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 29-AUG-1991 (first entry)

DB NS1_81-RlfAuth.

XX Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; KW influenza virus; non-structural protein 1; fusion.
 XX XX
 OS Plasmodium falciparum.
 INFLUENZA VIRUS; (A/PR/8/34).

RESULT 6 AARI7945 standard; protein; 319 AA.
 ID AARI7945 standard; protein; 319 AA.
 XX XX
 AC AARI7945;
 XX XX
 DT 25-MAR-2003 (revised)
 DT 22-FEB-1991 (first entry)
 XX DE NS181RlfAuth plasmid product.
 XX KW Malaria; vaccine.
 OS Plasmodium falciparum.
 XX Key Location/Qualifiers
 FT Domain 1..81
 /label= NS181 Protein Fragment
 /note= "from plasmid PMG-1"
 FT Domain 89..193
 /label= Fragment of circumsporozoite protein
 /note= "see comments"
 FT Domain 204..319
 /label= Fragment of circumsporozoite protein
 /note= "see comments"
 XX PN EP398540-A.
 XX

Location/Qualifiers
 FT Region 1..81
 /label= N-terminal of NS1
 /note= "Influenza virus nonstructural protein 1"
 FT Region 1..81
 /label= synthetic linker
 /note= "see comments"
 FT Region 89..193
 /label= AAS 19-123 of CS protein sequence
 /note= Region 1 contg. flanking region less signal sequence
 FT Region 194
 /label= artifact
 /note= "see comments"
 FT Region 195..319
 /label= AAS 288-412 of CS protein
 /note= Region II flanking region"

XX
PN EP432965-A.
XX
PD 19-JUN-1991.
XX
PF 06-DEC-1990; 90EP-00313257.
XX
PR 08-DEC-1989; 89US-00447746.
XX
PA (SMIK) SMITHKLINE BEECHAM.
PA (USSA) US SEC OF ARMY.
PA (BIOM) BIOMEDICAL RES INST.
PA (GROS/) GROSS M S.
XX
EI Gross MS, Gordon DM, Hollingdal MR;
XX
WPI: 1991-179771/25.
XX
Polypeptide comprising immunogenic determinants from P falciparum - for
PT vaccine against malaria infection in humans.
XX
BS Example 2: Page 10; 18pp; English.
XX
CC The polypeptide is preprod by genetic engineering of genes encoding the P.
CC falciparum circumsporozoite (CS) protein [Bane et al., Science 225 : 593
CC (1984)], and the influenza virus non-structural protein 1 (NS1), [Baez et
CC al., Nucleic Acids Research, 8 : 5845 (1980)]. The DNA encoding the 1st
CC 81 AAs of the N-terminal of NS1 (NS1_81) is linked via synthetic
CC signal sequence to DNA encoding Region I contg. flanking regions less the 18 AA
CC signal region, which in turn is fused to DNA encoding Region II-contg.
CC flanking region. This CS fusion is designated RfIAuth. The Pro residue
CC separating the ASP (at the C-terminal of the linker) from RfIAuth is an
CC artifact of a contg. filled in BamHI site; the Gly separating Region I and
CC Region II-contg. CS flanking regions is an artifact of a synthetic
CC FokI/RthII I linker. The peptide can be used in a vaccine for protection
CC against malaria. The complete nucleotide and AA sequences are given in EP
CC -304720, filed May 1, 1990. See also AARI13175-R13179.
CC (updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
CC standardise OS field.)
XX
SQ Sequence 319 AA;
Query Match Score 91; DB 2; Length 319;
Best Local Similarity 49.7%; Pred. No. 0.00012;
Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;
Qy 7 LRPGSSGSDL-----ERKIAKMEKASSVENVVNS 36
Db 268 IKPGSANPKDDEYNDIERKICRMKCSSVENVVNS 305
RESULT 8
AARI13177 ID AARI13177 standard; protein: 327 AA.
AC AARI13177;
XX DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 29-AUG-1991 (first entry)
XX
DB NS1_81-RfIAuth + (NANP)2.
XX
KW Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid;
KW influenza virus; non-structural protein 1; fusion.
OS Plasmodium falciparum.
OS Influenza virus; (A/PR/8/34/).
XX
Key Location/Qualifiers
1 -81
PT Region /label= N-terminal of NS1
FT /note= "Influenza virus nonstructural protein 1"
FT

PT Peptide 82. .87
PT FT /label= synthetic linker
88
PT Region /label= artifact
/note= "see comments"
89. .193 /label= AAs 19-123 of CS protein less signal
/note= "Region 1 contg. flanking region less signal
sequence"
194. .201 /label= immunodominant repeat region
/note= "two tetrapeptide repeat units"
202 /label= artifact
/note= "see comments"
203. .327 /label= AAs 288-412 of CS protein
/note= "Region II flanking region"
PT PT
XX BN432965-A.
XX
PD 19-JUN-1991.
XX
PF 06-DEC-1990; 90EP-00313257.
XX
PR 08-DEC-1989; 89US-00447746.
XX
PA (SMIK) SMITHKLINE BRECHAM.
PA (USSA) US SEC OF ARMY.
PA (BIOM) BIOMEDICAL RES INST.
PA (GROS/) GROSS M S.
XX
PI Gross MS, Gordon DM, Hollingdal MR;
DR W21; 1991-179771/25.
XX
Polypeptide comprising immunogenic determinants from P falciparum - for
PT vaccine against malaria infection in humans.
XX
Example 3: Page 10; 18pp; English.
XX
CC The polypeptide is preprod by genetic engineering of genes encoding the P.
CC falciparum circumsporozoite (CS) protein [Bane et al., Science 225 : 593
CC (1984)], and the influenza virus non-structural protein 1 (NS1), [Baez et
CC al., Nucleic Acids Research, 8 : 5845 (1980)]. The DNA encoding the 1st
CC 81 AAs of the N-terminal of NS1 (NS1_81) is linked via a synthetic
CC sequence to DNA encoding Region I contg. flanking regions less the 1 AA
CC signal region. This is linked to a synthetic sequence encoding two repeat
CC units from the immunodominant region, which in turn is fused to DNA
CC encoding Region II-contg. flanking region. The Pro residue separating the
CC ASP (at the C-terminal of the linker) from the Region I-contg. CS
flanking region is an artifact of a filled in BamHI site; the Gly
separating the repeat units and the Region II-contg. CS flanking region
is an artifact of a synthetic FokI/RthII I linker. The peptide can be
used in a vaccine for protection against malaria. See also AARI1306-
CC R12311 and AARI13175-R13179. (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 24-OCT-2003 to standardise OS field.)
XX
SQ Sequence 327 AA;
Query Match Score 91; DB 2; Length 319;
Best Local Similarity 49.7%; Pred. No. 0.00012;
Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;
Qy 7 LRPGSSGSDL-----ERKIAKMEKASSVENVVNS 36
Db 276 IKPGSANPKDDEYNDIERKICRMKCSSVENVVNS 313
RESULT 9
AARI-3178 ID AARI13178 standard; protein; 335 AA.
XX

PT vaccine against malaria infection in humans.

XX Example 5; Page 11; 18pp; English.

BS The polypeptide is prep'd. by genetic engineering of genes encoding the P.
 XX falciparum circumsporozoite (CS) protein [Dame et al., Science 225 : 593
 CC (1984)], and the influenza virus non-structural Protein 1 (NS1), [Baez et
 CC al., Nucleic Acids Research, 8 : 5845 (1980)]. The DNA encoding the 1st
 CC 81 AAs of the N-terminal of NS1 (NS1-81) is linked to a synthetic
 CC sequence encoding four repeat units (the variant form) from the
 CC immunodominant region, which in turn is linked via a synthetic sequence
 CC to DNA encoding Region I-contg. flanking region less the 18 AA signal
 CC region. This is linked to DNA encoding Region II-contg. flanking region.
 CC The Pro residue separating the Asp (the C-terminal of the linker) from
 CC the Region I-contg. CS flanking region is an artifact of a filled-in
 CC BamHI site; the Gly separating the Region I and II-contg. CS flanking
 CC regions is an artifact of a synthetic FokI/IrrHII I linker. The peptide
 CC can be used in a vaccine for protection against malaria. See also
 CC AAR1206-R12311 and AAR13175-113178. (Updated on 25-MAR-2003 to correct
 CC PA field.) (Updated on 24-OCT-2003 to standardise OS field)

XX Sequence 335 AA;

Query Match 49.7%; Score 91; DB 2; Length 335;
 Best Local Similarity 55.3%; Pred. No. 0.00013;
 Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

Qy 7 LRPGSSPSLSD-----EKIKAHRKASSVENVVNS 36
 Db 284 IKPGSANKPKPDKELDYENDIEKICKMEKCSSVENVVNS 321

XX Sequence 396 AA;

Query Match 49.7%; Score 91; DB 7; Length 396;
 Best Local Similarity 55.3%; Pred. No. 0.00015;
 Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

Qy 7 LRPGSSPSLSD-----EKIKAHRKASSVENVVNS 36
 Db 345 IKPGSANKPKPDKELDYENDIEKICKMEKCSSVENVVNS 362

XX Sequence 396 AA;

RESULT 11
 AAP83114
 ID AAP83114 standard; protein; 411 AA.
 XX
 AC AAP83114;
 AC AC
 DE Plasmodium falciparum.
 KW Vaccine; antigen; immunogen; probe; hybridisation; immunoassay;
 KW diagnosis.
 XX
 OS Plasmodium falciparum.
 XX
 FH Location/Qualifiers
 AC Key
 AC 106..120
 XX Region
 DT /note= "Region 1"
 XX
 DE 123..146
 XX Region
 FT /note= "Repeat region, repeat unit = NANPNVP"
 DE 147..206
 FT Region
 FT /note= "Repeat region, repeat unit = NANP"
 DE 211..286
 FT Region
 FT /note= "Repeat region, repeat unit = NANP"
 DE
 PN EP278940-A.
 XX
 PD 17-AUG-1988.
 XX
 PP 89EP-00870008.
 XX
 PR 25-JAN-1988;
 XX
 PR 30-JAN-1987;
 XX
 PA (SMIK) SMITH KLINE-RIT.
 PA (SKFK) SMITH KLINE-RIT.
 XX
 PI Cabazon T, De Wilde M, Harford N,
 XX
 DR WPI; 1988-229751/33.
 DR N-FSDB; AAN81108.

XX Encoding hepatitis B virus antigens and hybrids contg. them - used

XX DNA encoding hepatitis B virus antigens and bivalent vaccines.

XX Example; Fig 3AA-3AF; 101PP; English.

XX Sequence of the CS gene (AAN81108) is from lambda-mPF1. A recombinant DNA

XX molecule is claimed, comprising functional DNA coding sequence fused in

XX phase, to a portion of the Pre-S2 region of a hepatitis B virus (HBV) Pre

XX -S-S protein coding sequence. The functional DNA coding sequence

XX comprises the Pre-S2 coding sequence, Pre-S1 coding sequence or entire

XX Pre-S1-Pre-S2 coding sequence, the CS protein coding sequence of

XX a computational method which involves the calculation of several sequence

XX matching outlier protein sequences with protein sequences in databases.

XX Example 7; Page 44-45; 117pp; English.

XX The present invention relates to a method for identifying candidate

CC proteins in pathogens useful as anti-infectives. The invention discloses

CC a computational method which involves the calculation of several sequence

XX matching outlier protein sequences with protein sequences in databases.

XX Example 5; Page 11; 18pp; English.

XX Identifying candidate proteins useful as anti-infectives involves

XX matching outlier protein sequences with protein sequences in databases.

XX Sequence of the CS gene (AAN81108) is from lambda-mPF1. A recombinant DNA

XX molecule is claimed, comprising functional DNA coding sequence fused in

XX phase, to a portion of the Pre-S2 region of a hepatitis B virus (HBV) Pre

XX -S-S protein coding sequence. The functional DNA coding sequence

XX comprises the Pre-S2 coding sequence, Pre-S1 coding sequence or entire

XX Pre-S1-Pre-S2 coding sequence, the CS protein coding sequence of

CC attributes and their subsequence analysis results in the identification
 CC of outlier proteins in different pathogens. The method is useful for the
 CC identification of outlier proteins (e.g. virulence proteins, antigens or
 CC proteins used as drug targets) in pathogenic organisms. The method of the
 CC invention provides reproducible results as it does not depend on the
 CC variable biochemical characterisation of proteins. ABO23500-ABO3617
 CC represent outlier proteins identified from different pathogenic organisms
 XX

CC Sequence 396 AA;

Query Match 49.7%; Score 91; DB 7; Length 396;
 Best Local Similarity 55.3%; Pred. No. 0.00015;
 Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

Qy 7 LRPGSSPSLSD-----EKIKAHRKASSVENVVNS 36
 Db 345 IKPGSANKPKPDKELDYENDIEKICKMEKCSSVENVVNS 362

XX Sequence 396 AA;

RESULT 12
 AAP83114
 ID AAP83114 standard; protein; 411 AA.
 XX
 AC AAP83114;
 AC AC
 DE Plasmodium falciparum.
 KW Vaccine; antigen; immunogen; probe; hybridisation; immunoassay;
 KW diagnosis.
 XX
 OS Plasmodium falciparum.
 XX
 FH Location/Qualifiers
 AC Key
 AC 106..120
 XX Region
 DT /note= "Region 1"
 XX
 DE 123..146
 XX Region
 FT /note= "Repeat region, repeat unit = NANPNVP"
 DE 147..206
 FT Region
 FT /note= "Repeat region, repeat unit = NANP"
 DE 211..286
 FT Region
 FT /note= "Repeat region, repeat unit = NANP"
 DE
 PN EP278940-A.
 XX
 PD 17-AUG-1988.
 XX
 PP 89EP-00870008.
 XX
 PR 25-JAN-1988;
 XX
 PR 30-JAN-1987;
 XX
 PA (SMIK) SMITH KLINE-RIT.
 PA (SKFK) SMITH KLINE-RIT.
 XX
 PI Cabazon T, De Wilde M, Harford N,
 XX
 DR WPI; 1988-229751/33.
 DR N-FSDB; AAN81108.

XX DNA encoding hepatitis B virus antigens and hybrids contg. them - used
 XX DNA encoding hepatitis B virus antigens and bivalent vaccines.
 XX Example; Fig 3AA-3AF; 101PP; English.

CC Sequence of the CS gene (AAN81108) is from lambda-mPF1. A recombinant DNA
 CC molecule is claimed, comprising functional DNA coding sequence fused in
 CC phase, to a portion of the Pre-S2 region of a hepatitis B virus (HBV) Pre
 CC -S-S protein coding sequence. The functional DNA coding sequence
 CC comprises the Pre-S2 coding sequence, Pre-S1 coding sequence or entire
 CC Pre-S1-Pre-S2 coding sequence, the CS protein coding sequence of

Best Local Similarity 55.3%; Pred. No. 0.00017; 3; Mismatches 6; Indels 8; Gaps 1;

CC infections. The vaccines produce a humoral response and also a cellular immune response. (Updated on 25-MAR-2003 to correct. PN field.)

XX

SQ Sequence 424 AA;

Query Match 49.7%; Score 91; DB 21; Length 424;

CC Best Local Similarity 55.3%; Pred. No. 0.00017;

CC Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

CC

Qy 7 LRPSSCPSPSID-----EKKIARKEKASSVENVNS 36

DB 152 IKPGSANKPKDLDYANDIEKKICKNEKCSSVENVNS 189

RESULT 15

AAR37796

ID AAR37796 standard; protein; 424 AA.

XX

AC AAR37796;

XX

DT 25-MAR-2003 (revised)

DT 27-SEP-1993 (first entry)

XX

DE RTS protein.

XX

RN expression cassette; hybrid protein; *S. cerevisiae*; TDH3; cloning;

XX circumsporozoite protein; CSP; Plasmodium falciparum; strain 7G8;

XX hepatitis B virus; HBV; adv serotype; Pres2 protein; S protein.

XX

OS Synthetic.

XX

PH Key

FT Location/Qualifiers

Region 1 /note= "Derived from *S. cerevisiae* TDH3 gene sequence"

FT Region 2..4 /note= "Cloning artefact"

FT Protein 5..193 /note= "Represents amino acids 210-398 of the CSP of P.

FT falciparum."

FT Region 194..197 /note= "Carboxy terminal amino acids from HBV (adv serotype) pres2 protein"

FT Protein 198..424 /note= "S protein of HBV (adv serotype)"

FT /note= "S protein of HBV (adv serotype)"

XX WO9310152-A1.

DN XX

PD 27-MAY-1993.

XX 92WO-EP002591.

PF 11-NOV-1992;

XX 91GB-00024390.

PR 16-NOV-1991;

XX 92US-00842694.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX

PI De Wilde M, Cohen J;

XX DR 1993-18249/22.

DR N-PSDB; AA04256.

XX

PR Hybrid protein comprising Plasmodium circumsporozoite protein and HBsAg - useful as a vaccine for treating patients susceptible to Plasmodium infections.

XX Disclosure: Fig 5; 5pp; English.

XX This sequence represents the RTS hybrid protein which is encoded by the RTS expression cassette. This hybrid consists of a methionine residue derived from *S. cerevisiae* TDH3 gene sequence, three amino acids, Met-Ala -Pro, derived from a nucleotide segment created by the cloning procedure used to construct the hybrid gene, a stretch of 18 amino acids representing amino acids 210 to 398 of the circumsporozoite protein (CSP) of Plasmodium falciparum strain 7G8, an amino acid Arg created by the cloning procedure, four amino acids, Pro-Val-Thr-Asn, representing the four carboxy terminal residues of hepatitis B virus (HBV), adv serotype, Pres2 protein, and a stretch of 226 amino acids specifying the S protein of HBV, adv serotype. This protein, and RTS* (see also AAR7797), may be combined with an adjuvant and used in a vaccine for preventing plasmodium

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GenCore version 5.1.6

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.
 M Protein - protein search, using SW model
 run on: March 10, 2004, 09:16:59 ; Search time 28.2957 Seconds
 (without alignments)
 268.645 Million cell updates/sec
 title: US-09-848-834A-16
 perfect score: 183
 sequence: 1 XHWSYGLRPGSGPSLDEKKIAKMKASSVENVNS 36
 scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 searched: 809742 seqs, 211153259 residues
 total number of hits satisfying chosen parameters : 809742
 minimum DB seq length: 0
 maximum DB seq length: 2000000000
 post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries
 database: Published Applications AA:
 Sequence 1, APP
 Sequence 2, APP
 Sequence 3, APP
 Sequence 4, APP
 Sequence 5, APP
 Sequence 6, APP
 Sequence 7, APP
 Sequence 8, APP
 Sequence 9, APP
 Sequence 10, APP
 Sequence 11, APP
 Sequence 12, APP
 Sequence 13, APP
 Sequence 14, APP
 Sequence 15, APP
 Sequence 16, APP
 Sequence 17, APP
 Sequence 18, APP
 Sequence 19, APP
 Sequence 20, APP
 Sequence 21, APP
 Sequence 22, APP
 Sequence 23, APP
 Sequence 24, APP
 Sequence 25, APP
 Sequence 26, APP

ALIGNMENTS

RESULT 1
US-09-849-834A-16
Sequence 16, Application US/09849834A
; Patient No: US200407616A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Chimeric Peptide Immunogens
; FILE REFERENCE: 110-265-0447
; CURRENT APPLICATION NUMBER: US/09/849, 834A
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202, 328
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
SEQ ID NO: 16
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimeric Peptide consisting of amino acid sequence 1-10
; OTHER INFORMATION: RH hormone linked by a spacer to amino acid sequence 37-38
; OTHER INFORMATION: the Plasmodium falciparum circumsporozoite (CSP) protein
; NAME KEY: MOD-RES
; LOCATION: (1) - (1)
; OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline
; NAME KEY: PEPTIDE
; LOCATION: (1) - (10)
; OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
; NAME KEY: PEPTIDE
; LOCATION: (11) - (16)
; OTHER INFORMATION: Spacer peptide
; NAME KEY: PEPTIDE
; LOCATION: (17) - (36)
; OTHER INFORMATION: Amino acid sequence 378-398 of the Malaria
; OTHER INFORMATION: (Plasmodium falciparum) circumsporozoite (CSP) protein
; OTHER INFORMATION: US-09-849-834A-16

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ESTIMATES

result	Query				ID	Description
	No.	Score	Match	Length	DB	
1	182	99.5	36	9	US-09-848-834A-16	Sequence 16, APP1
2	182	99.5	51	9	US-09-848-834A-20	Sequence 20, APP1
3	95	51.9	20	9	US-09-848-834A-3	Sequence 3, APP1
4	95	51.9	33	9	US-09-848-834A-12	Sequence 12, APP1
5	91	49.7	396	10	US-09-820-834A-31	Sequence 31, APP1
6	89	48.6	19	14	US-09-239-31A-54	Sequence 54, APP1
7	89	48.6	21	10	US-09-932-165-1482	Sequence 1482, APP1
8	89	48.6	21	10	US-09-935-384-710	Sequence 710, APP1
9	89	48.6	21	10	US-09-942-052-11	Sequence 711, APP1
10	89	48.6	21	14	US-09-001-469-1404	Sequence 1404, APP1
11	89	48.6	21	14	US-10-128-711-97	Sequence 97, APP1
12	89	48.6	21	14	US-10-116-118-33	Sequence 33, APP1
13	89	48.6	21	14	US-10-062-109A-761	Sequence 761, APP1
14	89	48.6	21	14	US-10-005-480A-761	Sequence 761, APP1
15	89	48.6	21	14	US-10-277-292-652	Sequence 652, APP1

Query Match 99.5%; Score 182; DB 9; Length 36;
 Best Local Similarity 100.0%; Pred. No. 8.8e-19;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HWSYGLRPGSSGSLDEKKIARMKAKASSVENTVNS 36
 Db 2 HWSYGLRPGSSGSPSLDEKKIARMKAKASSVENTVNS 36

RESULT 2

FILE REFERENCE: 1102865-0047
 CURRENT APPLICATION NUMBER: US/09/848, 834A
 CURRENT FILING DATE: 2001-05-04
 PRIOR APPLICATION NUMBER: 60/202, 328
 NUMBER OF SEQ ID NOS: 20
 SEQ ID NO: 20
 LENGTH: 51

TYPE: PRT
 ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of human GnRH linked by a spacer to amino acid sequence 378-398 of Plasmodium falciparum circumsporozoite (CSP) protein

NAME/KEY: MOD_RES
 LOCATION: (1)..(1)
 OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline

NAME/KEY: MOD_RES
 LOCATION: (51)..(51)
 OTHER INFORMATION: Amidated glycine or Glycinamide

NAME/KEY: PEPTIDE
 LOCATION: (1)..(10)
 OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone

NAME/KEY: PEPTIDE
 LOCATION: (11)..(16)
 OTHER INFORMATION: Spacer peptide

NAME/KEY: PEPTIDE
 LOCATION: (17)..(36)
 OTHER INFORMATION: Amino acid sequence 378-398 of the Plasmodium falciparum circumsporozoite (CSP) protein

NAME/KEY: PEPTIDE
 LOCATION: (37)..(42)
 OTHER INFORMATION: Spacer peptide

NAME/KEY: PEPTIDE
 LOCATION: (43)..(51)
 OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone

CURRENT FILING DATE: 2001-05-04
 PRIOR APPLICATION NUMBER: 60/202, 328
 NUMBER OF SEQ ID NOS: 20
 SEQ ID NO: 20
 LENGTH: 20

TYPE: PRT
 ORGANISM: Plasmodium falciparum

FEATURE:
 NAME KEY: PEPTIDE
 LOCATION: (1)..(20)
 OTHER INFORMATION: Amino acid sequence 378-398 of the Plasmodium falciparum circumsporozoite (CSP) protein

US-09-848-834A-20
 Sequence 20, Application US/09848834A
 Patent No. US20020076416A1
 GENERAL INFORMATION:
 APPLICANT: Aphtron Corporation
 TITLE OF INVENTION: Chimeric Peptide Immunogens

FILE REFERENCE: 1102865-0047
 CURRENT APPLICATION NUMBER: US/09/848, 834A
 CURRENT FILING DATE: 2001-05-04
 PRIOR APPLICATION NUMBER: 60/202, 328
 NUMBER OF SEQ ID NOS: 20
 SEQ ID NO: 20
 LENGTH: 20

TYPE: PRT
 ORGANISM: Plasmodium falciparum

FEATURE:
 NAME KEY: PEPTIDE
 LOCATION: (1)..(20)
 OTHER INFORMATION: Amino acid sequence 378-398 of the Plasmodium falciparum circumsporozoite (CSP) protein

RESULT 4

US-09-848-834A-12

Sequence 12, Application US/09848834A

Patent No. US20020076416A1

GENERAL INFORMATION:

APPLICANT: Aphtron Corporation

TITLE OF INVENTION: Chimeric Peptide Immunogens

FILE REFERENCE: 1102865-0047

CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: 60/202, 328

NUMBER OF SEQ ID NOS: 20

SEQ ID NO: 20

LENGTH: 33

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 378-398 of th

OTHER INFORMATION: Plasmodium falciparum CSP protein linked by a spacer to amino ac

OTHER INFORMATION: id sequence 2-10 of the GnRH hormone

NAME/KEY: MOD_RES

LOCATION: (1)..(1)

OTHER INFORMATION: Amidated aspartic acid

NAME/KEY: MOD_RES

LOCATION: (33)..(33)

OTHER INFORMATION: Amidated glycine or glycaminide

NAME/KEY: PEPTIDE

LOCATION: (1)..(20)

OTHER INFORMATION: Amino acid sequence 378-398 of the Malaria

OTHER INFORMATION: (Plasmodium falciparum) circumsporozoite

(CSP) protein

NAME/KEY: PEPTIDE

LOCATION: (21)..(24)

OTHER INFORMATION: Spacer peptide

NAME/KEY: PEPTIDE

LOCATION: (25)..(33)

OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone

US-09-848-834A-12

Query Match 99.5%; Score 182; DB 9; Length 51;

Best Local Similarity 100.0%; Pred. No. 1.3e-18;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HWSYGLRPGSSGSLDEKKIARMKAKASSVENTVNS 36
 Db 2 HWSYGLRPGSSGSPSLDEKKIARMKAKASSVENTVNS 36

RESULT 3

US-09-848-834A-3

Sequence 3, Application US/09848834A

Patent No. US20020076416A1

GENERAL INFORMATION:

APPLICANT: Aphtron Corporation

TITLE OF INVENTION: Chimeric Peptide Immunogens

FILE REFERENCE: 1102865-0047

CURRENT APPLICATION NUMBER: US/09/848, 834A

RESULT 5
US-09-820-843A-31
Sequence 31, Application US/09820843A
Publication No. US2003039963A1
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820, 843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 31
LENGTH: 396
TYPE: PRT
ORGANISM: Plasmodium falciparum
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Circumsporozoite (CS) protein
NAME/KEY: misc_feature
OTHER INFORMATION: 91|4493889
US-09-820-843A-31

Query Match 49.7%; Score 91; DB 10; Length 396;
Best Local Similarity 55.3%; Pred. No. 0.00015; DB 10; Length 396;
Matches 21; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

Qy 7 LRPSSPSLSD-----EKKIAKNEKASSVENVNS 36
Db 345 IKPGSANKPKDLDYANDIEKKICMKCSSVENVNS 382

RESULTS 6
US-10-239-313A-54
Sequence 54, Application US/10239313A
Publication No. US2003017525A1
GENERAL INFORMATION:
APPLICANT: KLINGEUR - HAMOUR, Christine
APPLICANT: CORVAIL, Nathalie
APPLICANT: BECK, Alain
APPLICANT: GOETSCH, Liliane
APPLICANT: KLINGEUR - HAMOUR, Christine
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
FILE REFERENCE: 343 727 - US
CURRENT APPLICATION NUMBER: US/10/239, 313A
PRIORITY FILING DATE: 2002-09-19
PRIORITY APPLICATION NUMBER: FR 00/03711
PRIORITY FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 697
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 54
LENGTH: 19
TYPE: PRT
ORGANISM: Plasmodium malariae
US-10-239-313A-54

Query Match 48.6%; Score 89; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e-06; DB 14; Length 19;
Matches 0; Mismatches 0; Indels 0; Gaps 0;

RESULTS 7
US-09-932-165-1482

RESULT 9
 Sequence 711, Application US/09942052
 Publication No. US20030170626A1
 GENERAL INFORMATION:
 APPLICANT: Raitano, Arthur B.
 APPLICANT: Paris, Mary
 APPLICANT: Hubert, Rene S.
 APPLICANT: Afar, Daniel
 APPLICANT: Ge, Waigmao
 APPLICANT: Challita-Eid, Pia M.
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
 FILE REFERENCE: 51158-20028.00
 CURRENT APPLICATION NUMBER: US/09/942,052
 CURRENT FILING DATE: 2001-08-28
 PRIOR APPLICATION NUMBER: 60/228,432
 PRIOR FILING DATE: 2000-08-28
 NUMBER OF SEQ ID NOS: 744
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 711
 LENGTH: 21
 TYPE: PRT
 ORGANISM: Plasmodium falciparum
 US-09-942-052-711

Query Match 48.6%; Score 89; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.3e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EKKIAKMEKASSVFTVNS 36
 Db 3 EKKIAKMEKASSVFTVNS 21

RESULT 10
 Sequence 1,04, Application US/10001469
 Publication No. US20030091562A1
 GENERAL INFORMATION:
 APPLICANT: JAKOBOWITS, AYA
 APPLICANT: RAITANO, ARTHUR
 APPLICANT: AFAR, DANIEL
 APPLICANT: SAFFRAN, DOUGLAS
 APPLICANT: HUBERT, RENE
 APPLICANT: PARIS, MARY
 APPLICANT: CHALLITA-EID, PIA
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 1012PA1 USEFUL IN TREATMENT AND DETECTION OF CANCER
 FILE REFERENCE: 51158-20024.20
 CURRENT APPLICATION NUMBER: US/10/001,469
 CURRENT FILING DATE: 2003-05-20
 PRIOR APPLICATION NUMBER: 60/157,902
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: 60/231,118
 PRIOR FILING DATE: 2001-05-15
 PRIOR APPLICATION NUMBER: 09/680,728
 PRIOR FILING DATE: 2000-10-05
 NUMBER OF SEQ ID NOS: 2888
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 1404
 LENGTH: 21
 TYPE: PRT
 ORGANISM: Plasmodium falciparum
 US-10-001-469-1404

Query Match 48.6%; Score 89; DB 14; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.3e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EKKIAKMEKASSVFTVNS 36
 Db 3 EKKIAKMEKASSVFTVNS 21

RESULT 12
US-10-116-118-33
; Sequence 33, Application US/10116118
; Publication No. US2003014367A1
; GENERAL INFORMATION:
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn
; APPLICANT: Fikes, John D.
; TITLE OF INVENTION: Heterocyclic Analogs and Related Methods
; CURRENT APPLICATION NUMBER: US/10/116.118
; CURRENT FILING DATE: 2002-08-07
; PRIORITY APPLICATION NUMBER: US 60/166,529
; PRIOR FILING DATE: 1999-11-18
; PRIORITY APPLICATION NUMBER: US 60/239,048
; PRIOR FILING DATE: 2001-10-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 33
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
; US-10-116-118-33

Query Match 48.6%; Score 89; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EKKIAKMEKASSVNVNS 36
Db 3 EKKIAKMEKASSVNVNS 21

RESULT 13
US-10-062-109A-761
; Sequence 761, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Chalita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Enitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062.109A
; CURRENT FILING DATE: 2002-01-31
; PRIORITY APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 761
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-062-109A-761

Query Match 48.6%; Score 89; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EKKIAKMEKASSVNVNS 36
Db 3 EKKIAKMEKASSVNVNS 21

RESULT 14
US-10-005-480A-761
; Sequence 761, Application US/10005480A
; Publication No. US2003019107A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Chalita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Enitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 761
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-005-480A-761

Query Match 48.6%; Score 89; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EKKIAKMEKASSVNVNS 36
Db 3 EKKIAKMEKASSVNVNS 21

RESULT 15
US-10-2-292-652
; Sequence 652, Application US/10277292
; Publication No. US2003019470A1
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene
; APPLICANT: Raitano, Arthur
; APPLICANT: Afar, Daniel
; APPLICANT: Levitt, Elana
; APPLICANT: Chalita-Bid, Pia
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEAR ACID AND CORRESPONDING PROTEIN NAMED 118P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20105.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIORITY APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIORITY APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-09-22
; PRIORITY APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 652
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
; US-10-277-292-652

Query Match 48.6%; Score 89; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EKKIAKMEKASSVNVNS 36
Db 3 EKKIAKMEKASSVNVNS 21

Db 3 EKKIARMEKASSVENVNS 21

Search completed: March 10, 2004, 10:25:49
Job time : 28.2957 secs

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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 12.0019 Seconds

(without alignments)
133.345 Million cell updates/sec

Title: US-09-848-834A-15

Perfect score: 162 XHPSYGLRPQSSGPSLQYIKANSKFIGITEL 31

Sequence: scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cggn2_6/ptcdatal2/iaa/5A_COMB_Pep:
 2: /cggn2_6/ptcdatal2/iaa/5B_COMB_Pep:
 3: /cggn2_6/ptcdatal2/iaa/6A_COMB_Pep:
 4: /cggn2_6/ptcdatal2/iaa/6B_COMB_Pep:
 5: /cggn2_6/ptcdatal2/iaa/PCTUSCOMB_Pep:
 6: /cggn2_6/ptcdatal2/iaa/backfile1_Pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	51.9	24	4 US-09-164-088-6	Sequence 6, Appli
2	84	51.9	24	4 PCT-US9207218-31	Sequence 6, Appli
3	78	48.1	182	4 US-09-196-219-4	Sequence 4, Appli
4	77	47.5	173	4 US-09-162-731A-13	Sequence 13, Appli
5	76	46.9	17	4 US-08-472-701-23	Sequence 34, Appli
6	76	46.9	17	5 PCT-US55-08956-23	Sequence 1, Appli
7	76	46.9	31	5 PCT-US93-11703-63	Sequence 55, Appli
8	76	46.9	37	1 US-08-446-632-57	Sequence 69, Appli
9	76	46.9	37	1 US-08-446-632-63	Sequence 57, Appli
10	76	46.9	37	2 US-08-488-311A-57	Sequence 63, Appli
11	76	46.9	37	2 US-08-488-311A-63	Sequence 15, Appli
12	76	46.9	47	1 US-08-446-692-35	Sequence 14, Appli
13	76	46.9	47	2 US-08-488-311A-35	Sequence 13, Appli
14	76	46.9	853	4 US-08-913-880C-13	Sequence 12, Appli
15	76	46.9	858	4 US-08-913-880C-16	Sequence 11, Appli
16	76	46.9	860	4 US-08-913-880C-15	Sequence 10, Appli
17	76	46.9	862	4 US-08-913-880C-14	Sequence 9, Appli
18	76	46.9	865	4 US-08-913-880C-13	Sequence 8, Appli
19	76	46.9	866	4 US-08-913-880C-12	Sequence 7, Appli
20	76	46.9	874	4 US-08-913-880C-11	Sequence 6, Appli
21	76	46.9	875	4 US-08-913-880C-10	Sequence 5, Appli
22	76	46.9	1315	4 US-08-913-880C-1	Sequence 4, Appli
23	74	45.7	15	2 US-08-319-704-10	Sequence 3, Appli
24	74	45.7	15	2 US-08-661-012-6	Sequence 2, Appli
25	74	45.7	15	2 US-08-661-052-7	Sequence 1, Appli
26	74	45.7	15	3 US-09-046-313-2	Sequence 0, Appli
27	74	45.7	15	3 US-09-188-082-6	Sequence 0, Appli

ALIGNMENTS

RESULT 1
US-08-446-496-31
; Sequence 31, Application US/08464496
; Patent No. 6327789
; GENERAL INFORMATION:
; APPLICANT: Epimmune, Inc.
; APPLICANT: Vitello, Maria
; APPLICANT: Chasnut, Robert W.
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
; FILE REFERENCE: 33963-2001-13
; CURRENT APPLICATION NUMBER: US/08/464,496
; PRIOR APPLICATION NUMBER: 07/935,811
; PRIOR FILING DATE: 1992-08-26
; PRIOR NUMBER: 07/874,491
; PRIOR FILING DATE: 1992-04-27
; PRIOR APPLICATION NUMBER: 07/827,682
; PRIOR FILING DATE: 1992-01-29
; PRIOR APPLICATION NUMBER: 07/749,568
; PRIOR FILING DATE: 1991-08-26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 31
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligopeptide
US-08-446-496-31

Query Match Score 51.9%; Best Local Similarity 77.3%; Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 9 PGSGSPSQYIKANSKFIGITE 30
Db 3 PSDFFPSQYIKANSKFIGITE 24

RESULT 2
PCT-US9207218-31
; Sequence 31, Application PC/TUS9207218
; GENERAL INFORMATION:
; APPLICANT: Vitello, Maria A.
; APPLICANT: Chasnut, Robert W.
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
; NUMBER OF INVENTION: EPITOPE
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07218
FILING DATE: 1992-08-26
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REGISTRATION/DOCKET NUMBER: 14137-26-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-346-2400
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: AMINO ACID
STRANGENESS: single
TOPROLOGY: linear
MOLECULE TYPE: protein

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Query Match      48.1%; Score 78; DB 4; Length 182;
Best Local Similarity 81.0%; Pred. No. 0.00053; Mismatches 3; Indels 0; Gaps 0;
Matches 17; Conservative 1; MisMatches 3; Indels 0; Gaps 0;
Query      11 SSGPSIQLQYIKANSKRPDIGITL 31
Db       107 SSHNLMQYIKANSKRPDIGITEL 127

RESULT 4
US-09-396-937-18
; Sequence 18, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
;   APPLICANT: M&E Biotech A/S
;   APPLICANT: HALKIER, Torben
;   APPLICANT: HAANING, Jesper
;   TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
;   FILE REFERENCE: 22021 PC 1
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 173
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion between
; OTHER INFORMATION: murine OPGL, residues 158-316 with tetanus toxoid
; OTHER INFORMATION: P2 epitope introduced, and His tag
US-09-396-937-18

Query Match      47.5%; Score 77; DB 4; Length 173;
Best Local Similarity 66.1%; Pred. No. 0.00077; Mismatches 4; Indels 4; Gaps 1;
Matches 18; Conservative 1; MisMatches 4; Indels 4; Gaps 1;
Query      5 YGLRPGGSPGSTLOYIKANSKRPDIGITL 31
Db       137 FKURGEE---QYIKANSKRPDIGITEL 159

RESULT 5
US-08-472-701-23
; Sequence 23, Application US/08472701
; Patent No. 6500165
; GENERAL INFORMATION:
;   APPLICANT: Griffin, Ann C.
;   APPLICANT: Griffin, William F.
;   TITLE OF INVENTION: Detection and Treatment Methods for
;   TITLE OF INVENTION: Type I Diabetes
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: LARIVE S COCKFIELD
;     STREET: 60 State Street, suite 510
;     CITY: Boston
;     STATE: Massachusetts
;     COUNTRY: USA
;     ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/472-701
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/272,220
;     FILING DATE: 08-MAY-1994

```

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: DeConti, Giulio A., Jr.
 REGISTRATION NUMBER: 31,503
 REFERENCE/DOCKET NUMBER: DCI-032DV
 TELEPHONE: (617)227-7400
 TELECOMMUNICATION INFORMATION:
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 amino acids
 TYPE: amino acid
 TOPOLGY: linear
 MOLECULE TYPE: Peptide
 FRAGMENT TYPE: internal
 US-08-472-701-23

Query Match 46.9%; Score 76; DB 4; Length 17;
 Best Local Similarity 93.8%; Pred. No. 7e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LOYIKANSKFIGITEL 31
 Db 2 MOYIKANSKFIGITEL 17

RESULT 6 PCT-US95-08596-23
 Sequence 23, Application PC/TUS9508596
 GENERAL INFORMATION:
 APPLICANT: Proinsulin Peptide Compounds for Detecting
 TITLE OF INVENTION: Proinsulin Peptide Compounds for Detecting
 TITLE OF INVENTION: and Treating Type I Diabetes
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: PCT/US95/08596
 FILING DATE:
 CLASIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/272,220
 FILING DATE: 08-JULY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: DeConti, Giulio A., Jr.
 REGISTRATION NUMBER: 31,503
 REFERENCE/DOCKET NUMBER: DCI-032PC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 amino acids
 TYPE: amino acid
 TOPOLGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 PCT-US95-08596-23

Query Match 46.9%; Score 76; DB 5; Length 17;
 Best Local Similarity 93.8%; Pred. No. 7e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LOYIKANSKFIGITEL 31
 Db 2 MOYIKANSKFIGITEL 17

RESULT 7 PCT-US93-11703-63
 Sequence 63, Application PC/TUS9311703
 GENERAL INFORMATION:
 APPLICANT: Chiron Mimotopes Pty. Ltd.
 TITLE OF INVENTION: T-Cell Epitopes
 NUMBER OF SEQUENCES: 75
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Grant D. Green
 STREET: 4560 Horton St.
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94608
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/11703
 FILING DATE: 28-DEC-1993
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/984,852
 FILING DATE: 07-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Green, Grant D.
 REGISTRATION NUMBER: 31,259
 REFERENCE/DOCKET NUMBER: 0222.101
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 510-601-2706
 TELEFAX: 510-555-3542
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US93-11703-63

Query Match 46.9%; Score 76; DB 5; Length 31;
 Best Local Similarity 93.8%; Pred. No. 0.00014;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LOYIKANSKFIGITEL 31
 Db 2 MOYIKANSKFIGITEL 17

RESULT 8 US-08-446-692-57
 Sequence 57, Application US/0844692
 Patent No. 5759551
 GENERAL INFORMATION:
 APPLICANT: Ladd, Anna
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Wang, Chang Yi
 APPLICANT: Zamb, Timothy
 TITLE OF INVENTION: Immunogenic LHRH Peptide constructs
 NUMBER OF SEQUENCES: 114
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Maria C.H. Lin
 STREET: 345 Park Avenue
 CITY: New York
 STATE: NY

COUNTRY: US
 ZIP: 10154-0053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/446,692
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Maria C. H. Lin
 REGISTRATION NUMBER: 29-323
 REFERENCE/DOCKET NUMBER: 1151-4146 US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)415-8745
 TELEFAX: (516)751-6849
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 37 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-446-692-57

RESULT 10
 Query Match 46.9%: Score 76; DB 1; Length 37;
 Best Local Similarity 84.2%; Pred. No. 0.00017;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 13 GPSIQQYIKANSKFIGITEL 31
 Db 17 GGKQYIKANSKFIGITEL 35

RESULT 10
 Sequence 57, Application US/08488351A
 Patent No. 584346
 GENERAL INFORMATION:
 APPLICANT: Ladd, Anna
 APPLICANT: Wang, Chang Yi
 APPLICANT: Zamb, Timothy
 TITLE OF INVENTION: Immunogenic LHRH peptide constructs
 TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
 NUMBER OF SEQUENCES: 114
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Maria C.H. Lin
 STREET: 345 Park Avenue
 CITY: New York
 STATE: NY
 COUNTRY: US
 ZIP: 10154-0053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: IBM PC compatible
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/488,351A
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/446,692
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/446,692
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/446,692
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/446,692
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Maria C.H. Lin
 REGISTRATION NUMBER: 29-323
 REFERENCE/DOCKET NUMBER: 1151-4146 US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)415-8745
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Maria C.H. Lin
 REGISTRATION NUMBER: 29-323
 REFERENCE/DOCKET NUMBER: 1151-4146 US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)415-8745
 TELEFAX: (516)751-6849
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 37
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-488-351A-57

Query Match 46.9%: Score 76; DB 2; Length 37;
 Best Local Similarity 84.2%; Pred. No. 0.00017;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 13 GPSIQQYIKANSKFIGITEL 31
 Db 17 GGKQYIKANSKFIGITEL 35

Db 17 GGKKQYIKANSKFIGITEL 35

RESULT 11

US-09-848-351A-63

Sequence 63, Application US/08488351A

Patent No. 5843446

GENERAL INFORMATION:

APPLICANT: Ladd, Anna

APPLICANT: Wang, Chang Yi

APPLICANT: Zamb, Timothy

TITLE OF INVENTION: Immunogenic LHRH Peptide constructs

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: Maria C.H. Lin

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: US

ZIP: 10154-0053

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,351A

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maria C.H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4146 US2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)415-7745

TELEFAX: (516)751-6849

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 47 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-446-692-35

RESULT 13

US-08-488-351A-35

Sequence 35, Application US/08488351A

Patent No. 5843446

GENERAL INFORMATION:

APPLICANT: Ladd, Anna

APPLICANT: Wang, Chang Yi

APPLICANT: Zamb, Timothy

TITLE OF INVENTION: Immunogenic LHRH Peptide constructs

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: Maria C.H. Lin

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: US

ZIP: 10154-0053

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,351A

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/446,692

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maria C.H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4146 US2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)415-7745

TELEFAX: (516)751-6849

INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-488-351A-63

RESULT 12

US-08-446-692-35

Sequence 35, Application US/08446692

Patent No. 5759551

GENERAL INFORMATION:

APPLICANT: Ladd, Anna

APPLICANT: Wang, Chang Yi

APPLICANT: Zamb, Timothy

TITLE OF INVENTION: Immunogenic LHRH peptide constructs

and synthetic universal immune stimulators for vaccines

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: Maria C.H. Lin

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: US

ZIP: 10154-0053

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,351A

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/446,692

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maria C.H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4146 US2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)415-7745

TELEFAX: (516)751-6849

INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-488-351A-63

RESULT 13

US-08-488-351A-35

Sequence 35, Application US/08488351A

Patent No. 5843446

GENERAL INFORMATION:

APPLICANT: Ladd, Anna

APPLICANT: Wang, Chang Yi

APPLICANT: Zamb, Timothy

TITLE OF INVENTION: Immunogenic LHRH peptide constructs

and synthetic universal immune stimulators for vaccines

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: Maria C.H. Lin

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: US

ZIP: 10154-0053

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,351A

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/446,692

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maria C.H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4146 US2

Patent No. 5843446

GENERAL INFORMATION:

APPLICANT: Ladd, Anna

APPLICANT: Wang, Chang Yi

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; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
;   APPLICATION NUMBER: US 08/229,275
;   FILING DATE: 14-APR-1994
;   CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
;   APPLICATION NUMBER: US 08/057,166
;   FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
;   NAME: Maria C.H. Lin
;   REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)415-8745
;   TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-488-351A-35

Query Match      46.9%;  Score 76;  DB 2;  Length 47;
Best Local Similarity  84.2%;  Pred. No. 0.00022;  Length 47;
Matches 16;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

Qy    16 GPQLQYIKANSKFIGITEL 31
Db    17 GGKKQYIKANSKFIGITEL 35

RESULT 14
US-08-913-880C-17
; Sequence 17, Application US/08913880C
; Patent No. 637225
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Morihiro
; TITLE OF INVENTION: TETANUS TOXIN FUNCTIONAL FRAGMENT ANTIGEN AND TETANUS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 216-380P
; CURRENT APPLICATION NUMBER: US/08/913,880C
; CURRENT FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 17
; LENGTH: 853
; TYPE: PRT
; ORGANISM: Clostridium tetani
; FEATURE:
; OTHER INFORMATION: Amino Acids 463 to 1315 of SEQ ID NO: 1
US-08-913-880C-17

Query Match      46.9%;  Score 76;  DB 4;  Length 853;
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Matches 15;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    16 LOYIKANSKFIGITEL 31
Db    367 MOYIKANSKFIGITEL 382

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; Sequence 16, Application US/08913880C
; Patent No. 637225
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Morihiro
; TITLE OF INVENTION: TETANUS TOXIN FUNCTIONAL FRAGMENT ANTIGEN AND TETANUS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 216-380P
; CURRENT APPLICATION NUMBER: US/08/913,880C
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GenCore version 5.1.6		P87167 schizosaccharomyces pombe
Copyright (c) 1993 - 2004 Compugen Ltd.		P51922 porichthys porochromi
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title: US-09-848-834A-15		Q39618 chlamydomonas
perfect score: 162		P24913 herpesvirus
sequence: 1 XHWSYGLRPGSSGGPSLQYIKANSKFIGITEL 31		Q9Z812 chlamydial pili
scoring table: BLOSUM62		P01747 clupea pallasi
GapOp 10.0 , Gapext 0.5		P01746 mus musculus
searched: 141681 seqs, 52070155 residues		P01746 mus musculus
total number of hits satisfying chosen parameters:	141681	
minimum DB seq length: 0		
maximum DB seq length: 2000000000		
post-processing: Minimum Match 0%		
Maximum Match 100%		
Listing first 45 summaries		
database : SwissProt_42::*		
Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
		SUMMARIES
result No.	Score	Query Match Length DB ID Description
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3	60	37.0 61 1 GONI_SHEEP
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8	58	35.8 91 1 GONI_TIG
9	58	35.8 92 1 GONI_HUMAN
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RL	Bur. J. Biochem.	188:39-45 (1990).
RN	[6]	InterPro; IPR000395; Peptidase_M27;
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RX	MEDLINE=92317619; PubMed=1935979;	DR; PRINTS; PRO00760; BONTOXILYSIN.
RA	Kriegstein K.G., Henschke A.H.,	DR; PRODom; PD001963; Bontoxilysin; 1.
RA	"Limited proteolysis of tetanus toxin. Relation to activity and identification of cleavage sites.";	DR; PROSITE; PS00142; ZINC PROTEASE; 1.
RT	RT	KW; Neurotoxin; Transmembrane: Hydrolase; Metalloprotease; Zinc; Plasmid;
RT	RT	KW; 3D-Structure; Complete proteome.
RL	RN	FT INIT_MET 0 0 TETANUS TOXIN LIGHT CHAIN.
RP	IDENTIFICATION AS ZINC-PROTEASE.	FT CHAIN 1 456 TETANUS TOXIN HEAVY CHAIN.
RA	Schiavo G., Poulin B., Rossetto O., Benfenati F., Teac L.,	FT METAL 232 ZINC (CATALYTIC) (BY SIMILARITY).
RA	Montecucco C.,	FT ACT SITE 233 BY SIMILARITY.
RA	"Tetanus toxin is a zinc protein and its inhibition of neurotransmitter release and protease activity depend on zinc.";	FT TRANSMEM 226 ZINC (CATALYTIC) (BY SIMILARITY).
RT	RT	FT DISULFID 438 POTENTIAL.
RL	EMBO J. 11:3577-3583(1992).	FT DISULFID 1076 1092 INTERCHAIN.
RN	RN	FT IDENTIFICATION OF SUBSTRATE.
RX	MEDLINE=93010918; PubMed=396558	FT TURN 876 882
RA	Schiavo G., Poulin B., Rossetto O., de Laureto P.P.,	FT STRAND 883 883
RA	Dasgupta B.R., Montecucco C.,	FT TURN 884 891
RA	"Tetanus and borulium-B neurotoxins block neurotransmitter release by proteolytic cleavage of synaptobrevin.";	FT STRAND 892 893
RT	RT	FT STRAND 894 897
RT	RT	FT TURN 904 907
RT	RT	FT TURN 909 910
RL	Nature 359:832-835(1992).	FT STRAND 912 915
RN	RN	FT STRAND 920 925
RX	X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 874-1314.	FT TURN 928 929
RA	MEDLINE=97475217; PubMed=334741;	FT STRAND 932 935
RA	Umland T.C., Winger L.M., Swaminathan S., Furey W.F., Schmidt J.J.,	FT HELIX 938 940
RA	Sax M.;	FT TURN 941 946
RT	"Structure of the receptor binding fragment HC of tetanus neurotoxin.";	FT STRAND 949 956
RT	Nat. Struct. Biol. 4:788-792(1997).	FT HELIX 962 968
CC	-1- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPROTEIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GUN- -PHE-77 BOND OF SYNAPTOBREVIN-2.	FT TURN 969 970
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of 76-Gln- -Phe-77 bond in synaptobrevin 2.	FT STRAND 972 977
CC	-1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).	FT STRAND 980 981
CC	-1- SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO YIELD SUBCHAINS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDGE AND ARE NON-TOXIC AFTER SEPARATION	FT HELIX 983 985
CC	-1- MISCELLANEOUS: THIS C-TERMINAL OF THE HEAVY CHAIN BINDS TO GANGLIOSIDE RECEPTORS.	FT TURN 987 995
CC	-1- SIMILARITY: Belongs to peptidase family M27.	FT STRAND 996 997
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CC	--	FT STRAND 1006 1007
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CC	--	FT STRAND 1127 1131
DR	EMBL; AF528097; AAO3754.1; -.	FT HELIX 1132 1134
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DR	PDB; 1AF9; 29-APR-98.	FT TURN 1144 1145
DR	PDB; 1ABD; 14-OCT-98.	FT STRAND 1148 1152
DR	PDB; 1DOH; 27-MAR-00.	FT TURN 1155 1158
DR	PDB; 1DFQ; 24-MAR-00.	FT STRAND 1159 1162
DR	PDB; 1DIW; 24-MAR-00.	FT STRAND 1163 1166
DR	PDB; 1DII; 24-MAR-00.	FT STRAND 1173 1178
DR	PDB; 1FV3; 05-SEP-01.	FT TURN 1184 1185
DR	MEROPS; M27_001; -.	FT STRAND 1188 1190
DR	InterPro; IPR002150; Pept M_Zn_Bs.	FT STRAND 1190 1190
DR	InterPro; IPR006025; ConA_like_lec_g1.	FT STRAND 1190 1190

Db	Qy	Query Match	Score	DB 1;	Length	1314;	
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		DT	15-DEC-1998	(Rel. 37, Last annotation update)	DT	15-DEC-1998 (Rel. 41, Last annotation update)	
		DT	28-FEB-2003	(Rel. 41, Last annotation update)	DT	28-FEB-2003 (Rel. 41, Last annotation update)	
		DE	Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)]		DE	Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)]	
		DE	(Luteinizing hormone-releasing hormone I)		DE	(Luteinizing hormone-releasing hormone I)	
		DE	(GnRH I) (Lutiberin I); GnRH-associated peptide I]		DE	(Lutiberin I) (Lutiberin I); GnRH-associated peptide I]	
		GN	GNRH OR GNRH OR LHRH.		GN	GNRH OR GNRH OR LHRH.	
		OC	Mesocricetus auratus (Golden hamster).		OS	Ovis aries (Sheep).	
		OC	Mesocricetus auratus; Chorodata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.		OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.	
		NCBI_TaxID	91940;		RN	[1]	
		RN	SEQUENCE OF 12-61 FROM N.A.		RP	SEQUENCE OF 12-61 FROM N.A.	
		RN	STRAIN=Western range; TISSUE=Hypothalamus;		RC	STRAIN=Western range; TISSUE=Hypothalamus;	
		RA	Burgus R., Butcher M., Amos M., Ling N., Monahan M., Rivier J.,		RA	Burgus R., Butcher M., Amos M., Ling N., Monahan M., Rivier J.,	
		RA	Fellows R., Blackwell R., Vale W., Guillen M.R., Guillen R.J.		RA	Fellows R., Blackwell R., Vale W., Guillen M.R., Guillen R.J.	
		RT	"Primary structure of the ovine hypothalamic luteinizing hormone-releasing factor (LRF) (LH-hypothalamus-LRF gas chromatography-mass spectrometry-decapeptide-Edman degradation)." (See http://www.ncbi.nlm.nih.gov/pubmed/13721972).		RT	"Primary structure of the ovine hypothalamic luteinizing hormone-releasing factor (LRF) (LH-hypothalamus-LRF gas chromatography-mass spectrometry-decapeptide-Edman degradation)." (See http://www.ncbi.nlm.nih.gov/pubmed/13721972).	
		RT	Proc. Natl. Acad. Sci. U.S.A. 69:278-282 (1972).		RT	Proc. Natl. Acad. Sci. U.S.A. 69:278-282 (1972).	
		RL	Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.		RL	Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.	
		RN	[2]		RN	[1]	
		RP	SEQUENCE OF 1-10.		RP	SEQUENCE OF 1-10.	
		RX	MEDLINE:72094314; PubMed:45505058;		RX	MEDLINE:72094314; PubMed:45505058;	
		RA	Burgus R., Butcher M., Amos M., Ling N., Monahan M., Rivier J.,		RA	Burgus R., Butcher M., Amos M., Ling N., Monahan M., Rivier J.,	
		RA	Fellows R., Blackwell R., Vale W., Guillen M.R., Guillen R.J.		RA	Fellows R., Blackwell R., Vale W., Guillen M.R., Guillen R.J.	
		CC	--!- SIMILARITY: Belongs to the GnRH family.		CC	--!- SIMILARITY: Belongs to the GnRH family.	
		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. The statement is long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ncbi.nlm.nih.gov/announce/ or send an email to license@ibb-sib.ch).	
		CC	--!- SUBCELLULAR LOCATION: Secreted.		CC	--!- SUBCELLULAR LOCATION: Secreted.	
		CC	--!- SIMILARITY: Belongs to the GnRH family.		CC	--!- SIMILARITY: Belongs to the GnRH family.	
		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. The statement is long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ncbi.nlm.nih.gov/announce/ or send an email to license@ibb-sib.ch).		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. The statement is long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ncbi.nlm.nih.gov/announce/ or send an email to license@ibb-sib.ch).	
		CC	--!- FUNCTION: Stimulates the secretion of both luteinizing and follicle-stimulating hormones.		CC	--!- FUNCTION: Stimulates the secretion of both luteinizing and follicle-stimulating hormones.	
		CC	--!- FUNCTION: Stimulates the secretion of both luteinizing and follicle-stimulating hormones.		CC	--!- FUNCTION: Stimulates the secretion of both luteinizing and follicle-stimulating hormones.	
		CC	--!- PROSITE: IPRO01541; GONADOLIBRNI.		CC	--!- PROSITE: IPRO01541; GONADOLIBRNI.	
		DR	InterPro; IPR002012; Gnrh.		DR	InterPro; IPR002012; Gnrh.	
		DR	InterPro; IPR004079; GonadoliberinI.		DR	InterPro; IPR004079; GonadoliberinI.	
		DR	PRINTS; PRO01541; GONADOLIBRNI.		DR	PRINTS; PRO01541; GONADOLIBRNI.	
		DR	PROSITE; PS00446; Gnrh.		DR	PROSITE; PS00446; Gnrh.	
		KW	Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;		KW	Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;	
		CC	Placenta; Pyrrolidone carboxylic acid.		CC	Placenta; Pyrrolidone carboxylic acid.	
		FT	NON_TER	1	FT	NON_TER	1
		FT	PROGONADOLIBERIN I.		FT	PROGONADOLIBERIN I.	
		FT	GONADOLIBERIN I.		FT	GONADOLIBERIN I.	
		FT	GNRH ASSOCIATED PEPTIDE I (BY SIMILARITY).		FT	GNRH ASSOCIATED PEPTIDE I (BY SIMILARITY).	
		FT	ACT_SITE	3	FT	ACT_SITE	3
		FT	APPEARS TO BE ESSENTIAL FOR BIOLOGICAL ACTIVITY (BY SIMILARITY).		FT	APPEARS TO BE ESSENTIAL FOR BIOLOGICAL ACTIVITY (BY SIMILARITY).	
		FT	MOD_RES	1	FT	MOD_RES	1
		FT	PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).		FT	PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).	
		FT	MOD_RES	10	FT	MOD_RES	10
		FT	AMIDATION (G-11 PROVIDE AMIDE GROUP) (BY SIMILARITY).		FT	AMIDATION (G-11 PROVIDE AMIDE GROUP) (BY SIMILARITY).	
		FT	NON_TER	63	FT	NON_TER	61
		SQ	SEQUENCE	63 AA;	SQ	SEQUENCE	61 AA;
			7370 MW;			63965AA1AE319B8F0 CRC64;	
			FC9499567F77180 CRC64;				
		Query Match	37.7%	Score 61;	DB 1;	Length 63;	
		Best Local Similarity	46.2%	Pred. No.	0.023;		
		Matches 12;	Conservative	3;	Mismatches	3;	
		Indels	8;	Gaps	1;		
		Indels	2;	Mismatches	1;		
		Indels	8;	Gaps	1;		
		Query Match	37.0%	Score 60;	DB 1;	Length 61;	
		Best Local Similarity	52.2%	Pred. No.	0.032;		
		Matches 12;	Conservative	1;	Mismatches	2;	
		Indels	8;	Gaps	1;		
		Query Match	2 HWSYGLRPSSGGPSLQYIKANSKEFIG 27				
		Best Local Similarity	46.2%	Pred. No.	0.023;		
		Matches 12;	Conservative	3;	Mismatches	3;	
		Indels	8;	Gaps	1;		
		Query Match	2 HWSYGLRPSSGGPSLQYIKANSKEFIG 24				
		Best Local Similarity	52.2%	Pred. No.	0.032;		
		Matches 12;	Conservative	1;	Mismatches	2;	
		Indels	8;	Gaps	1;		

Db 2 HWSYGLRPGG-----KRNAAK 16

RESULT 4		RESULT 5	
GONI_RANCA	STANDARD;	PRT;	90 AA.
ID_GONI_RANCA			
AC Q90Y63;			
DD 10-OCT-2003 (Rel. 42, Created)			
DT 10-OCT-2003 (Rel. 42, Last sequence update)			
DT 10-OCT-2003 (Rel. 42, Last annotation update)			
DE Progonadotropin I precursor (Contains: Gonadotropin I (LHRH I))			
DE Luteinizing hormone releasing hormone I (Gonadotropin-releasing hormone I) (GnRH I) (Liberin I); GnRH-associated peptide I (GAP1).			
DE GNRH1 OR GNRH.			
OS Rana catesbeiana (Bull Frog).			
OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi; Amphibia; Batracia; Anura; Neobatrachia; Ranidae; Rana.			
OX NCBI_TaxID=8440;			
RN [1]			
RC TISSUE_Brain;			
XX MEDLINE21102951; PubMed=11170016;			
RA Wang L., Yoo M.S., Kang H.M., Im W.B., Choi H.S., Bogerd J., Kwon H.B.;			
RT "Cloning and characterization of cDNAs encoding the GnRH1 and GnRH2 precursors from bullfrog (Rana catesbeiana).";			
RL J. Exp. Zool. 289:190-201 (2001).			
CC -!- FUNCTION: Stimulates the secretion of gonadotropins (By similarity).			
CC -!- SUBCELLULAR LOCATION: Secreted.			
CC -!- TISSUE SPECIFICITY: Forebrain.			
CC -!- DEVELOPMENTAL STAGE: Expressed at significantly higher levels during post-breeding. Not expressed in pituitary.			
CC -!- SIMILARITY: Belongs to the GnRH family.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC DR APF8754; AA05972.1; -.			
DR GO:GO:0005716; C:extracellular; NAS.			
DR GO:GO:0005189; Plutein-releasing factor activity; NAS.			
DR GO:GO:0009755; P:hormone mediated signaling; NAS.			
DR PRINTER; PS000003; Preparation; NAS.			
DR InterPro; IPRO002012; GrRH.			
DR InterPro; IPRO00079; Gonadotropin.			
DR PF00446; Gnrh_1.			
DR PRNTMS; PRO1541; GONADOLIBRN1.			
DR PROSITE; PS00473; GrRH.			
KW Pyrrolidone carboxylic acid.			
FT SIGNAL 1 24 POTENTIAL.			
FT CHAIN 25 90 PROGONADOLIBERIN I.			
FT PEPTIDE 25 34 GONADOLIBERIN I.			
FT PEPTIDE 38 86 GNRH-ASSOCIATED PEPTIDE I (BY SIMILARITY).			
FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).			
FT MOD_RES 34 34 AMIDATION (G-35 PROVIDE AMIDE GROUP) (BY SIMILARITY).			
FT SEQUENCE 90 AA; 10291 MW; 317203BAE3DA2FE7 CRC64;			
FT SEQUENCE 90 AA; 10291 MW; 317203BAE3DA2FE7 CRC64;			
Query Match 36.7%; Score 59.5; DB 1; Length 90;			
Best Local Similarity 47.1%; Pred. No. 0.06;			
Matches 16; Conservative 4; Mismatches 9; Indels 5; Gaps 3;			
Qy 2 HWSYGLRPGSG--PSLQ--YIRANSKFGITEL 31			
Db 26 HWSYGLRPGSKREVESSLQESYAEVNE-VSFTEL 58			
Query Match 35.8%; Score 58; DB 1; Length 67;			
Best Local Similarity 100.0%; Pred. No. 0.071; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy 2 HWSYGLRPG 10			
Db 7 HWSYGLRPG 15			

CC EMBL; X01059; CAA25526.1; .
DR EMBL; M12578; AAA3516.1; .
DR PIR; S05308; RHHUG.
DR Gene; HGNC:4119; GNRH1.
MIM; 1152760; .
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0005183; P:luteneinizing hormone-releasing factor activity; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR InterPro; IPR002012; GnRH.
DR InterPro; IPR004079; Gonadoliberin1.
DR PRINTS; PF00446; GnRH; 1.
DR PROSITE; PS00473; GNRH; 1.
DR Clavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
Placenta; Pharmaceutical; Signal; Polymorphism;
KRN Pyrrolidone carboxylic acid.
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT PEPTIDE; 24 33 GNRH ASSOCIATED PEPTIDE I.
FT ACT_SITE; 37 92 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY.
FT MOD_RES; 26 26 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES; 24 24 AMIDATION (G->4 PROVIDE AMIDE GROUP).
FT VARIANT; 33 33 W -> S (In dbSNP: 6.85).
FT VARIANT; 16 16 /FTID:VAR_013943.
SQ SEQUENCE 92 AA; 10380 MW; 30A/2221B076FA79 CRC64;

Query Match 35.8%; score 58; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;
Indels 0; FT PRT; 92 AA.

2 HWSYGLRP 10
Db 25 HWSYGLRP 33

RESULT 10
ID GONI_RAT STANDARD; PRT; 92 AA.
AC P07490;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Progonadoliberin I Precursor (Contains: Gonadoliberin I (LH-RH I)
DE (Luteneinizing hormone hormone I) (Gonadotropin-releasing
hormone I) (GnRH I) (Luliberin I); Prolactin release-inhibiting Factor
DE II).
DN GNRH1 OR GNRH.
OS Battus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID:1011; .
RN SEQUENCE FROM N.A.
RP MEDLINE=86034333; PubMed=867548;
RA Adelman J.P.; Mason A.J.; Hayfllick J.S.; Seeburg P.H.;
RT "Isolation of the gene and hypothalamic cDNA for the common precursor
RT of Gonadotropin-releasing hormone and Prolactin release-inhibiting
RT factor in human and rat";
RN Proc. Natl. Acad. Sci. U.S.A. 83:179-183 (1986).
RL [1] SEQUENCE FROM N.A.
R2 ID GONI_TUPGB STANDARD; PRT; 92 AA.
AC Q9535;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Progonadoliberin I Precursor (Contains: Gonadoliberin I (LH-RH I)
DE (Luteneinizing hormone-releasing hormone I) (Gonadotropin-releasing

[3]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE=92105410; PubMed=1463115;
RA Maier C.C.; Marchetti B.; Leboeuf R.D.; Blalock J.E.;
RT "Thymocytes express a mRNA that is identical to hypothalamic
RT luteinizing hormone-releasing hormone mRNA.",
RL Cell. Mol. Neurobiol. 12:447-454 (1992).
RN [4]
RN SEQUENCE OF 1-47 FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=87149087; PubMed=3547652;
RA Adelman J.P.; Bond C.T.; Douglass J.J.; Herbert E.;
RT "Two mammalian genes transcribed from opposite strands of the same
DNA locus";
RL Science 235:154-157 (1987).
CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
the secretion of both luteinizing and follicle-stimulating
hormones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Belongs to the Gnrh Family.
CC -1- SIMILARITY: Belongs to the Gnrh Family.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC DR S50870; AAB24572.1; -
EMBL; M12579; AAA41263.1; -
DR EMBL; M31670; AAA41264.1; -
DR M15527; AAA42141.1; ALT SEQ.
DR EMBL; M15539; AAA42139.1; -
DR M15528; -; NOT_ANNOTATED_CDS.
DR PIR; A40147; RHTG12.
DR InterPro; IPR002012; GnRH.
DR InterPro; IPR004079; Gonadoliberin1.
DR PTam; PF00446; GnRH; 1.
DR PRINTS; PRO1541; GONADOLIBERN1.
DR PROSITE; PS00472; GNRH; 1.
DR KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
KW Placenta; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT DEPTIDE; 24 33 GONADOLIBERIN I.
FT PEPTIDE; 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
FT ACT_SITE; 26 26 APPARENTS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY.
FT FT PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES; 24 24 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SEQ; 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT DEPTIDE; 24 33 GONADOLIBERIN I.
FT PEPTIDE; 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
FT ACT_SITE; 26 26 APPARENTS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY.
FT FT PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES; 24 24 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SEQ; 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT DEPTIDE; 24 33 GONADOLIBERIN I.
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FT SEQ; 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT DEPTIDE; 24 33 GONADOLIBERIN I.
FT PEPTIDE; 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
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FT MOD_RES; 24 24 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SEQ; 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT DEPTIDE; 24 33 GONADOLIBERIN I.
FT PEPTIDE; 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
FT ACT_SITE; 26 26 APPARENTS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY.
FT FT PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES; 24 24 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SEQ; 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT DEPTIDE; 24 33 GONADOLIBERIN I.
FT PEPTIDE; 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
FT ACT_SITE; 26 26 APPARENTS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY.
FT FT PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES; 24 24 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SEQ; 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT DEPTIDE; 24 33 GONADOLIBERIN I.
FT PEPTIDE; 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
FT ACT_SITE; 26 26 APPARENTS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY.
FT FT PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES; 24 24 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SEQ; 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT DEPTIDE; 24 33 GONADOLIBERIN I.
FT PEPTIDE; 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
FT ACT_SITE; 26 26 APPARENTS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY.
FT FT PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES; 24 24 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SEQ; 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT DEPTIDE; 24 33 GONADOLIBERIN I.
FT PEPTIDE; 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
FT ACT_SITE; 26 26 APPARENTS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY.
FT FT PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES; 24 24 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SEQ; 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT DEPTIDE; 24 33 GONADOLIBERIN I.
FT PEPTIDE; 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
FT ACT_SITE; 26 26 APPARENTS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY.
FT FT PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES; 24 24 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SEQ; 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT DEPTIDE; 24 33 GONADOLIBERIN I.
FT PEPTIDE; 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
FT ACT_SITE; 26 26 APPARENTS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY.
FT FT PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES; 24 24 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SEQ; 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT DEPTIDE; 24 33 GONADOLIBERIN I.
FT PEPTIDE; 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
FT ACT_SITE; 26 26 APPARENTS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY.
FT FT PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES; 24 24 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SEQ; 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT DEPTIDE; 24 33 GONADOLIBERIN I.
FT PEPTIDE; 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
FT ACT_SITE; 26 26 APPARENTS TO BE ESSENTIAL FOR BIOLOGICAL
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FT MOD_RES; 24 24 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SEQ; 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT DEPTIDE; 24 33 GONADOLIBERIN I.
FT PEPTIDE; 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
FT ACT_SITE; 26 26 APPARENTS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY.
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FT SEQ; 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
FT CHAIN; 24 92 GONADOLIBERIN I.
FT DEPTIDE; 24 33 GONADOLIBERIN I.
FT PEPTIDE; 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
FT ACT_SITE; 26 26 APPARENTS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY.
FT FT PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES; 24 24 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SEQ; 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT SIGNAL; 1 23 PROGNADOLIBERIN I.
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FT ACT_SITE; 26 26 APPARENTS TO BE ESSENTIAL FOR BIOLOGICAL

DE hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide I].
 OS Tupaia glis belangeri (Common tree shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Scandentia; Tupaidida; Tupaia.
 OX NCBI_TAXID=37347;

[1] RN SEQUENCE FROM N.A.
 TISSUE:Hypothalamus;
 RXN MEDLINE=97079639; PubMed=8021350;
 PIA Kasten T.L., White S.A., Norton T.T., Bond C.T., Adelman J.P.,
 Fernald R.D.;
 RT "Characterization of two new preprodRH mRNAs in the tree shrew:
 first direct evidence for mesencephalic GnRH gene expression in a
 placental mammal";
 RT Gen. Comp. Endocrinol. 104:7-19(1996).
 CC -!- FUNCTION: Stimulates the secretion of Gonadotropins; it stimulates
 the secretion of both luteinizing and Follicle-Stimulating
 hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GnRH family.

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 or send an email to license@isb-sib.ch).

CC DR EMBL: U53326; AAB16837; 1; -
 DR InterPro; IPR002012; GnRH.
 DR Pfam: PF00446; GONADOLIBRINI.
 DR PRINTS: PRO1541; GONADOLIBRINI.
 DR PS00473; GNRH; 1.
 KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 KW Placenta; Signal; Pyrrolidone carboxylic acid.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT CHAIN 24 92 PROGONADOLIBRIN I.
 FT PEPTIDE 24 33 GONADOLIBERIN I.
 FT PEPTIDE 37 92 GNRH-ASSOCIATED PEPTIDE I.
 FT ACT_SITE 26 26 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
 FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
 FT SIMILARITY). AMIDATION (G-34 PROVIDE AMIDE GROUP) (BY
 FT SIMILARITY).
 FT MOD_RES 33 33 4FDBF2258CF5F63B CRC64;
 SQ SEQUENCE 92 AA; 10197 MW;

Query Match 35.8%; Score 58; DB 1; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 2 HWSYGLRP 10
 Db 25 HWSYGLRP 33

RESULT 12
 ID VGB4_BPM5 STANDARD; PRT; 66 AA.
 AC Q05511;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DR Gene 84 protein (GP84).
 GN 84.
 OS Mycobacteriophage L5.
 OS Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC L5-like viruses.
 OX NCBI_TAXID=31575;

RESULT 13
 ID GONI_ALMI STANDARD; PRT; 10 AA.
 AC P37041; P20407;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gondoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH I)
 DE (Luliberin I).
 OS Alligator mississippiensis (American alligator).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylia; Alligatorinae; Alligator.
 RN [1]; TAXID=8496;
 RN SEQUENCE;
 RXN TISSUE=Brain;
 MEDLINE=11352338; PubMed=1882082;
 RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
 RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
 RA "Primary structure of two forms of gonadotropin-releasing hormone
 from brains of the American alligator (Alligator mississippiensis)." ;
 RT Regul. Pept. 33:105-116(1991).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GnRH family.
 CC PIR: A60066; RHAQI.
 DR InterPro; IPR002012; GnRH.
 DR Pfam: PF00446; GnRH; 1.
 DR PROSITE; PS00073; GNRH; 1.
 RW Hormone; Amidation; Pyrothalamus; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MCD_BES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1172 MW;

Query Match 33.3%; Score 54; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.031; Indels 0; Gaps 0;
 Matches 8; Conservative 1; MisMatches 0; Indels 0;

QY 2 HWSYGLRP 10
 Db 2 HWSYGLQP 10
 2 HWSYGLQP 10

RESULT 14
 GONI_CHICK

DR PIR; I50739; I50739.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0005183; F:luteinizing hormone-releasing factor activity; NAS.
 DR GO; GO:0007275; P:development; IDA.
 DR InterPro; IPR002012; GnrH.
 DR InterPro; IPR04079; GonadoliberinI.
 DR Pfam; PF00446; GnrH; 1.
 DR PRINTS; PR01541; GONADOLIBRIN.
 DR PROSITE; PS00443; GNRH; 1.
 DR KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 KW Signal; Multigene family; Pyrrolidone carboxylic acid.
 PT SIGNAL 1 22
 PT CHAIN 23 94
 PT PEPTIDE 23 32
 PT PEPTIDE 36 94
 PT MOD_RES 23 23
 PT MOD_RES 32 32
 PT CONFLICT 86 94 MW;
 SQ SEQUENCE 94 AA; 10382 MW; E57DBA8333327BD7 CRC64;
 Query Match 32.1%; Score 52; DB 1; Length 94;
 Best Local Similarity 88.9%; Pred. No. 0.84;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 RMSYGLPFG 10
 Db 24 RMSYGLSSFG 32

Search completed: March 10, 2004, 09:13:57
 Job time : 6.66926 secs

Run on:	March 10, 2004, 08:58:54 ; Search time 30.6381 Seconds (without alignment) 319.245 Million cell updates/sec				
Title:	US-09-848-834A-15				
Perfect score:	162				
Sequence:	1 XHWSYGLRPSSGSPSIQYIKANSKFIGITBL 31				
Scoring table:	BLOSUM62				
Gapop:	10.0 , Gapext 0.5				
Searched:	1017041 seqs, 315518202 residues				
Total number of hits satisfying chosen parameters:	1017041				
Minimum DB seq length: 0					
Maximum DB seq length: 2000000000					
Post-processing: Minimum Match 0%					
Maximum Match 100%					
Database :	SPTREMBL_25;*				
	1: SP_archaea;*				
	2: SP_bacteria;*				
	3: SP_fungi;*				
	4: SP_hexebrate;*				
	5: SP_invertebrate;*				
	6: SP_mammal;*				
	7: SP_muc;*				
	8: SP_organelle;*				
	9: SP_phage;*				
	10: SP_plant;*				
	11: SP_rhodent;*				
	12: SP_virus;*				
	13: SP_vertebrate;*				
	14: SP_unclassified;*				
	15: SP_xvirus;*				
	16: SP_xbacteria;*				
	17: SP_archeap;*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
1	76	46.9	1310	2 Q93N27	Q93n27 clostridium anguilla ja
2	59	36.4	91	13 Q9PRHO	Q9PRHO anguilla ja
3	53	33.0	374	16 Q9YR6	Q9YR6 rhabdium m
4	53	32.7	308	16 Q883K3	Q883K3 pseudomonas
5	53	32.7	358	17 Q8TZU8	Q8TZU8 pyrococcus
6	52.5	32.4	214	16 Q8BTH5	Q8BTH5 streptococc
7	52.5	32.4	214	16 Q8E219	Q8E219 streptococc
8	52.5	32.4	437	16 Q8XKM3	Q8XKM3 clostridium
9	52	32.1	64	13 Q8JIF3	Q8JIF3 dentex dent
10	52	32.1	64	13 Q8JTF2	Q8JTF2 pigrus majo
11	52	32.1	68	13 Q8JFV4	Q8JFV4 acanthopagrus
12	52	32.1	87	13 Q9YI26	Q9YI26 sparis aura
13	52	32.1	94	13 Q8JFY3	Q8JFY3 oreochromis
14	52	32.1	96	13 Q8W80	Q8W80 verasper mo
15	52	32.1	98	13 Q805A5	Q805A5 oreochromis
16	52	32.1	120	13 Q7T059	Q7T059 micropogoni
17	51	31.5	208	16 Q8YR98	Q8YR98 anabaena sp
	51	31.5	1545	16 Q9R01	Q9R01 streptomyce
	50.5	31.2	1494	11 Q88902	Q88902 ratulus norv
	20	30.9	192	10 Q8LG49	Q8LG49 arabidopsis
	21	30.9	215	11 Q8CT5	Q8CT5 mus musculus
	22	30.9	224	6 Q2BB48	Q2BB48 smintthopsis
	23	30.9	341	12 Q8051	Q8051 yaba monkey
	24	30.9	575	17 Q8TS33	Q8TS33 methanosa
	25	30.9	1331	10 Q9SE13	Q9SE13 arabidopsis
	26	30.9	1379	10 Q84R20	Q84R20 arabidopsis
	27	49.5	30.6	13 Q9W05	Q9W05 oncorhynchus
	28	49.5	30.6	100 Q8GA23	Q8GA23 bifidobacter
	29	49.5	30.6	114 Q855P9	Q855P9 mycobacteri
	30	49.5	30.6	1485 Q8CIW4	Q8CIW4 syncytiacyst
	31	49.5	30.6	144 Q8UK61	Q8UK61 agrobacteri
	32	49	30.2	75 Q8UT51	Q8UT51 mycobacteri
	33	49	30.2	240 Q7U0Q2	Q7U0Q2 methanosa
	34	49	30.2	301 Q8TH52	Q8TH52 methanosa
	35	49	30.2	402 Q8VY65	Q8VY65 arabidopsis
	36	49	30.2	444 Q8FD37	Q8FD37 escherichia
	37	49	30.2	444 Q83Q25	Q83Q25 shigella fl
	38	49	30.2	448 Q83B26	Q83B26 coxiella bu
	39	49	30.2	481 Q50210	Q50210 melittangiu
	40	49	30.2	532 Q96671	Q96671 drosophila
	41	49	30.2	532 Q9VU53	Q9VU53 drosophila
	42	49	30.2	574 Q8TRV2	Q8TRV2 methanosa
	43	49	30.2	618 Q8PB96	Q8PB96 xanthomonas
	44	49	30.2	619 Q8PKS0	Q8PKS0 xanthomonas
	45	49	30.2	1047 Q9P6E3	Q9P6E3 neurospora
ALIGNMENTS					
RESULT 1					
ID	Q93N27	PRELIMINARY;	PRT;	1310 AA.	
AC	Q93N27				
DT	01-DEC-2001 (TREMBLref.)	19, Created)			
DT	01-DEC-2001 (TREMBLref.)	19, Last sequence update)			
DT	01-OCT-2003 (TREMBLref.)	25, Last annotation update)			
DE	Tetanus toxin (Fragment).				
OS	Clostridium tetani.				
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;				
OX	Clostridium.				
NCBI_TaxID=1513;					
[1]					
RN		SEQUENCE FROM N.A.			
RA		Shumin Z., Dianliang L.,			
RT		"Cloning and sequence analysis of tetanus toxin gene."			
RL		Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.			
DR	AF389424; AAK72964; -				
DR	GO-0004866; F: endopeptidase inhibitor activity; IEA.				
DR	GO-0008237; F: metallopeptidase inhibitor activity; IEA.				
DR	GO-0015070; F: toxin activity; IEA.				
DR	GO-0009405; P: pathogenesis; IEA.				
DR	GO-0008537; P: metallopeptidase inhibitor activity; IEA.				
DR	GO-0008270; F: zinc ion binding; IEA.				
DR	GO-0004858; P: proteolysis and peptidolysis; IEA.				
DR	InterPro; IPR008385; ConA-like lect_g1.				
DR	InterPro; IPR001064; Crystallin.				
DR	InterPro; IPR002160; Kuniz1 legume.				
DR	InterPro; IPR000395; Peptidase_M27.				
DR	InterPro; IPR000625; Pept M_Zn_BS.				
DR	Pfam; PF01742; Peptidase_M27; 1.				
DR	PFAM; PF01742; Peptidase_M27; 1.				
DR	ProDom; PDO01963; Bontoxilysin.				
DR	Prosite; PS00225; CRYSTALLIN_BETA_GAMMA; 1.				
DR	Prosite; PS00142; ZINC_Protease; 1.				
FT	NON_TER	1			
FT	NON_TER	1310 AA,			
SQ	SEQUENCE	1310 AA,			
Query Match		9EADDCC914416E450 CRC54;			
		46.9%; Score 76; DB 2; Length 1310;			

Qy	3 WSYGLRPGSSGSPSQYTIKANSKFIG 27	DR PRINTS; PRO0413; HADHALGNASE.
Db	234 WIVETFGGGEGNRYSELKFIG 258	DR TIGRFAMS; TIGR01509; HAD-SF-IA-v3; 1.
		KW Hypothetical protein; Complete proteome.
		SQ SEQUENCE 214 AA; 24470 MW; 7EB227E7BDB946854 CRC64;
RESULT 5		Query Match 32.4%; Score 52.5%; DB 16; Length 214;
OBJTIZB	PRELIMINARY;	Best Local Similarity 42.4%; Pred. No. 16;
ID		Mismatches 3; Indels 5; Gaps 2;
OBJTIZB	PRELIMINARY;	Matches 14; Conservative
AC	PRT; 358 AA.	
DT		
DT	01-JUN-2002 (TREMBLrel. 21, Created)	
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
DE	Glycosyl transferase.	
GN	Pyrococcus furiosus.	
OS	Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;	
OC	Pyrococcus.	
OX	[1]	
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A. PRELIMINARY; PRT; 214 AA.
RC	STRAIN=PC1 / DSM 3638 / ATCC 43567 / JCM 8422;	ID Q8E219; Q8E219;
RA	Weiss R. B., Dunn D.M., Robb F.T., Brown J.R.;	AC 01-MAR-2003 (TREMBLrel. 23, Created)
RT	"The complete sequence of the Pyrococcus furiosus genome.";	DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
RR	Submitted (PPB-2000) to the EMBL/GenBank/DBJ databases.	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DR	EMBL; AE010283; AAL82009; 1; -	
DR	GO; GO:0016740; PTtransferase activity; IEA.	
DR	GO; GO:0009058; P: Biosynthesis; IEA.	
DR	InterPro: IP0001296; Glyco trans 1.	
DR	PFam; PF00534; Glycos_transf_1.	
DR	Transfere; Complete genome.	
DR	SEQUENCE 358 AA; 40003 MW; 4D1FAA206B9F8A3C CRC64;	
Query Match 32.7%; Score 53; DB 17; Length 358;		
Best Local Similarity 52.6%; Pred. No. 24;		
Mismatches 4; Indels 0; Gaps 0;		
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;		
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;		
Qy	12 SGPSLOQYTIKANSKFIGITE 30	Query Match 32.4%; Score 52.5%; DB 16; Length 214;
Db	214 SGEPNLPEQDQAKRLGIEE 232	Best Local Similarity 42.4%; Pred. No. 16;
		Mismatches 3; Indels 5; Gaps 2;
RESULT 6		Matches 14; Conservative
Q8E7H5	PRELIMINARY;	
ID	PRT; 214 AA.	
Q8E7H5	PRELIMINARY;	
AC	PRT; 214 AA.	
DT	01-MAR-2003 (TREMBLrel. 23, Created)	
DT	01-JUN-2003 (TREMBLrel. 23, Last sequence update)	
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
DE	Hypothetical protein.	
GN	Streptococcus agalactiae (serotype III).	
OS	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	
OC	Streptococcus agalactiae (serotype III).	
OX	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=NE0316 / Serotype III;	
RC	MEDLINE=22242508; PubMed=1574221;	
RX	Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,	
RA	Msadek T., Zouine M., Couve E., Laloui L., Poyart C., Trieu-Cuot P.,	
RA	Kunst F.;	
RT	"Genome sequence of Streptococcus agalactiae, a pathogen causing RT invasive neonatal disease.";	
RT	Mol. Microbiol. 45:1499-1513 (2002).	
DR	EMBL; AL76844; CAD05824; 1; -	
DR	Sagalist, Gbs0179;	
DR	GO; GO:0016787; P: Hydrolase activity; IEA.	
DR	GO; GO:00081152; P: metabolism; IEA.	
DR	InterPro: IPRO06402; HAD-SF-IA-v3.	
DR	InterPro: IPRO05833; Hydrolase.	
DR	InterPro: IPRO05834; Hydrolase.	
PFam; PF00702; Hydrolase; 1.		
DR	PRINTS; PRO0411; HADHALGNASE.	
DR	TIGRFAMS; TIGR01509; HAD-SF-TA-v3; 1.	
DR	Complete proteome.	
DR	SEQUENCE 214 AA; 24470 MW; 7EB227E7BDB946854 CRC64;	
Query Match 32.4%; Score 52.5%; DB 16; Length 214;		
Best Local Similarity 42.4%; Pred. No. 16;		
Mismatches 3; Indels 5; Gaps 2;		
Matches 14; Conservative		
Qy	2 HW---SGYLREGSGPSLQYIANSKFIGITE 30	RESULT 8
Db	96 HWLHQHGYPLAVASSSPMVDF-IKRNLKELVATE 127	OBXKM3
		PRELIMINARY; PRT; 437 AA.
		ID OBXKM3;
		AC OBXKM3;
		DT 01-MAR-2002 (TREMBLrel. 20, Created)
		DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
		DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
		DE Probable sodium-and-chloride-dependent transporter.

GN CPE1371 OS Clostridium perfringens. Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; OC Clostridium. NCBI_TaxID=1502;	Qy 2 HWSYGLRPG 10 Db 16 HWSYGLSPG 24
RN [1] RP SEQUENCE FROM N.A. STRAIN=13 / Type A. RC MEDLINE=2164373; PubMed=11792847; RA Shimizu T., Ohtani K., Ohshima K., Yamashita A., Hirakawa H., Hayashi S., Kuhara M., Hattori M., Kuroda "Complete genome sequence of Clostridium perfringens, an anaerobic RT flesh-eater."; RT Gonadotropin-releasing hormone (Fragment). RL Pagrus major (Red sea bream) (Chrysophrys major). DR Bokuryoata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae; OC Sparidae; Pagrus. DR NCBI_TaxID=143350;	RESULT 10 QB1JF2 PRELIMINARY; PRT; 64 AA. ID QB1JF2; AC QB1JF2; DT 01-OCT-2002 (TREMBLrel. 22, Created) RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR GO; GO:0003183; P:fluteinizing hormone-releasing factor activity; IEA. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR GO; GO:0007275; P:development; IEA. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR InterPro; IPR000012; GnRH. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR InterPro; IPR004079; Gonadoliberini. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR InterPro; IPR00416; GnRH; 1. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR PRINTS; PRO1541; GONADOLIBRNI. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR PROSITE; PS00473; GnRH; 1. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR NON_TER 64 AA; 6967 MW; 119F0D0CD14BB6D0 CRC64;
GN CPE1371 OS Clostridium perfringens. Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; OC Clostridium. NCBI_TaxID=1502;	Qy 2 HWSYGLRPG 10 Db 16 HWSYGLSPG 24
RN [1] RP SEQUENCE FROM N.A. STRAIN=13 / Type A. RC MEDLINE=2164373; PubMed=11792847; RA Shimizu T., Ohtani K., Ohshima K., Yamashita A., Hirakawa H., Hayashi S., Kuhara M., Hattori M., Kuroda "Complete genome sequence of Clostridium perfringens, an anaerobic RT flesh-eater."; RT Gonadotropin-releasing hormone (Fragment). RL Pagrus major (Red sea bream) (Chrysophrys major). DR Bokuryoata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae; OC Sparidae; Pagrus. DR NCBI_TaxID=143350;	RESULT 9 QB1JF3 PRELIMINARY; PRT; 64 AA. ID QB1JF3; AC QB1JF3; DT 01-OCT-2002 (TREMBLrel. 22, Created) RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR GO; GO:0005576; P:fluteinizing hormone-releasing factor activity; IEA. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR InterPro; IPR004079; Gonadoliberini. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR InterPro; IPR00446; GnRH; 1. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR PRINTS; PRO1541; GONADOLIBRNI. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR PROSITE; PS00473; GnRH; 1. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR NON_TER 64 AA; 7028 MW; 1F91FFF2B4BB6D0 CRC64;
GN CPE1371 OS Clostridium perfringens. Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; OC Clostridium. NCBI_TaxID=1502;	Qy 2 HWSYGLRPG 10 Db 16 HWSYGLSPG 24
RN [1] RP SEQUENCE FROM N.A. STRAIN=13 / Type A. RC MEDLINE=2164373; PubMed=11792847; RA Shimizu T., Ohtani K., Ohshima K., Yamashita A., Hirakawa H., Hayashi S., Kuhara M., Hattori M., Kuroda "Complete genome sequence of Clostridium perfringens, an anaerobic RT flesh-eater."; RT Gonadotropin-releasing hormone (Fragment). RL Pagrus major (Red sea bream) (Chrysophrys major). DR Bokuryoata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae; OC Sparidae; Pagrus. DR NCBI_TaxID=143350;	RESULT 11 QB1JF4 PRELIMINARY; PRT; 68 AA. ID QB1JF4; AC QB1JF4; DT 01-OCT-2002 (TREMBLrel. 22, Created) RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR GO; GO:0005576; C:extracellular; IEA. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR InterPro; IPR004079; Gonadoliberini. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR InterPro; IPR00446; GnRH; 1. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR PRINTS; PRO1541; GONADOLIBRNI. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR PROSITE; PS00473; GnRH; 1. RN [1] RP SEQUENCE FROM N.A. RA Kato M., Elmseiray G.E.; RT "Sequence comparison of GnRH genes in closely-related Sparidae fishes"; DR NON_TER 64 AA; 64 MW; 1F91FFF2B4BB6D0 CRC64;

